

Nathan Wemmer

[Code ▼](#)

This is an R Markdown (<http://rmarkdown.rstudio.com>) Notebook. When you execute code within the notebook, the results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and pressing *Ctrl+Shift+Enter*.

Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.

When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).

The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*, *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor is displayed.

Chapter 4

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

[Hide](#)

```
worms <- read.table("worms.txt",header=T)
```

```
attach(worms)
names(worms)
```

```
[1] "Field.Name"  "Area"        "Slope"       "Vegetation"  "Soil.pH"     "Damp"        "Worm.density"
```

[Hide](#)

```
head(worms)
```

Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
1 Nashs.Field	3.6	11	Grassland	4.1	FALSE	4
2 Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
3 Nursery.Field	2.8	3	Grassland	4.3	FALSE	2

Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lg1>	Worm.density <int>
4 Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
5 Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6
6 Oak.Mead	3.1	2	Grassland	3.9	FALSE	2
6 rows						

Hide

tail(worms)

Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lg1>	Worm.density <int>
15 Pond.Field	4.1	0	Meadow	5.0	TRUE	6
16 Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
17 Cheapside	2.2	8	Scrub	4.7	TRUE	4
18 Pound.Hill	4.4	2	Arable	4.5	FALSE	5
19 Gravel.Pit	2.9	1	Grassland	3.5	FALSE	1
20 Farm.Wood	0.8	10	Scrub	5.1	TRUE	3
6 rows						

Hide

worms

Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lg1>	Worm.density <int>
Nashs.Field	3.6	11	Grassland	4.1	FALSE	4
Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
Nursery.Field	2.8	3	Grassland	4.3	FALSE	2
Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6
Oak.Mead	3.1	2	Grassland	3.9	FALSE	2
Church.Field	3.5	3	Grassland	4.2	FALSE	3
Ashurst	2.1	0	Arable	4.8	FALSE	4
The.Orchard	1.9	0	Orchard	5.7	FALSE	9

Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
1-10 of 20 rows					Previous	1 2 Next

Hide

summary(worms)

Field.Name	Area	Slope	Vegetation	Soil.pH	Damp
Worm.density					
Ashurst : 1	Min. :0.800	Min. : 0.00	Arable :3	Min. :3.500	Mode :logical
Min. :0.00					
Cheapside : 1	1st Qu.:2.175	1st Qu.: 0.75	Grassland:9	1st Qu.:4.100	FALSE:14
1st Qu.:2.00					
Church.Field: 1	Median :3.000	Median : 2.00	Meadow :3	Median :4.600	TRUE :6
Median :4.00					
Farm.Wood : 1	Mean :2.990	Mean : 3.50	Orchard :1	Mean :4.555	
Mean :4.35					
Garden.Wood : 1	3rd Qu.:3.725	3rd Qu.: 5.25	Scrub :4	3rd Qu.:5.000	
3rd Qu.:6.25					
Gravel.Pit : 1	Max. :5.100	Max. :11.00		Max. :5.700	
Max. :9.00					
(Other) :14					

Hide

by(worms,Vegetation,mean)

argument is not numeric or logical: returning NA
argument is not numeric or logical: returning NA
argument is not numeric or logical: returning NA
argument is not numeric or logical: returning NA

```
Vegetation: Arable
```

```
[1] NA
```

```
-----  
Vegetation: Grassland
```

```
[1] NA
```

```
-----  
Vegetation: Meadow
```

```
[1] NA
```

```
-----  
Vegetation: Orchard
```

```
[1] NA
```

```
-----  
Vegetation: Scrub
```

```
[1] NA
```

[Hide](#)

```
by(worms, Vegetation, function(x) lm(Worm.density ~ Soil.pH, data=x))
```

Vegetation: Arable

Call:

```
lm(formula = Worm.density ~ Soil.pH, data = x)
```

Coefficients:

(Intercept)	Soil.pH
-9.689	3.108

Vegetation: Grassland

Call:

```
lm(formula = Worm.density ~ Soil.pH, data = x)
```

Coefficients:

(Intercept)	Soil.pH
-15.041	4.265

Vegetation: Meadow

Call:

```
lm(formula = Worm.density ~ Soil.pH, data = x)
```

Coefficients:

(Intercept)	Soil.pH
31	-5

Vegetation: Orchard

Call:

```
lm(formula = Worm.density ~ Soil.pH, data = x)
```

Coefficients:

(Intercept)	Soil.pH
9	NA

Vegetation: Scrub

Call:

```
lm(formula = Worm.density ~ Soil.pH, data = x)
```

Coefficients:

(Intercept)	Soil.pH
4.4758	0.1613

Section 4.1

Hide

worms[3,5]

[1] 4.3

Hide

worms[14:19,7]

[1] 0 6 8 4 5 1

Hide

worms[1:5,2:3]

	Area <dbl>	Slope <int>
1	3.6	11
2	5.1	2
3	2.8	3
4	2.4	5
5	3.8	0
5 rows		

Hide

worms[3,]

Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
3 Nursery.Field	2.8	3	Grassland	4.3	FALSE	2
1 row						

Hide

worms[,3]

[1] 11 2 3 5 0 2 3 0 0 4 10 1 2 6 0 0 8 2 1 10

Hide

```
class(worms[3,])
```

```
[1] "data.frame"
```

Hide

```
class(worms[,3])
```

```
[1] "integer"
```

Hide

```
worms[,c(1,5)]
```

Field.Name	Soil.pH
<fctr>	<dbl>
Nashs.Field	4.1
Silwood.Bottom	5.2
Nursery.Field	4.3
Rush.Meadow	4.9
Gunness.Thicket	4.2
Oak.Mead	3.9
Church.Field	4.2
Ashurst	4.8
The.Orchard	5.7
Rookery.Slope	5.0
1-10 of 20 rows	
Previous 1 2 Next	

Hide

```
NA
```

Section 4.2

Hide

```
worms[sample(1:20,8),]
```

Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
<fctr>	<dbl>	<int>	<fctr>	<dbl>	<lgl>	<int>

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	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
2	Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
14	Observatory.Ridge	1.8	6	Grassland	3.8	FALSE	0
11	Garden.Wood	2.9	10	Scrub	5.2	FALSE	8
6	Oak.Mead	3.1	2	Grassland	3.9	FALSE	2
16	Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
19	Gravel.Pit	2.9	1	Grassland	3.5	FALSE	1
3	Nursery.Field	2.8	3	Grassland	4.3	FALSE	2
10	Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
8 rows							

Section 4.3

Hide

worms[order(Slope),]

	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
5	Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6
8	Ashurst	2.1	0	Arable	4.8	FALSE	4
9	The.Orchard	1.9	0	Orchard	5.7	FALSE	9
15	Pond.Field	4.1	0	Meadow	5.0	TRUE	6
16	Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
12	North.Gravel	3.3	1	Grassland	4.1	FALSE	1
19	Gravel.Pit	2.9	1	Grassland	3.5	FALSE	1
2	Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
6	Oak.Mead	3.1	2	Grassland	3.9	FALSE	2
13	South.Gravel	3.7	2	Grassland	4.0	FALSE	2
1-10 of 20 rows							Previous 1 2 Next

Hide

worms[rev(order(Slope)),]

	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
1	Nashs.Field	3.6	11	Grassland	4.1	FALSE	4
20	Farm.Wood	0.8	10	Scrub	5.1	TRUE	3
11	Garden.Wood	2.9	10	Scrub	5.2	FALSE	8
17	Cheapside	2.2	8	Scrub	4.7	TRUE	4
14	Observatory.Ridge	1.8	6	Grassland	3.8	FALSE	0
4	Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
10	Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
7	Church.Field	3.5	3	Grassland	4.2	FALSE	3
3	Nursery.Field	2.8	3	Grassland	4.3	FALSE	2
18	Pound.Hill	4.4	2	Arable	4.5	FALSE	5
1-10 of 20 rows							Previous 1 2 Next

Section 4.4

Hide

```
worms[Damp == T,]
```

	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
4	Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
10	Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
15	Pond.Field	4.1	0	Meadow	5.0	TRUE	6
16	Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
17	Cheapside	2.2	8	Scrub	4.7	TRUE	4
20	Farm.Wood	0.8	10	Scrub	5.1	TRUE	3
6 rows							

Hide

```
worms[Worm.density > median(Worm.density) & Soil.pH < 5.2,]
```

	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
4	Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5

Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
<fctr>	<dbl>	<int>	<fctr>	<dbl>	<lgl>	<int>
5 Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6
10 Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
15 Pond.Field	4.1	0	Meadow	5.0	TRUE	6
16 Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
18 Pound.Hill	4.4	2	Arable	4.5	FALSE	5

6 rows

Hide

worms[,sapply(worms,is.numeric)]

Area	Slope	Soil.pH	Worm.density
<dbl>	<int>	<dbl>	<int>
3.6	11	4.1	4
5.1	2	5.2	7
2.8	3	4.3	2
2.4	5	4.9	5
3.8	0	4.2	6
3.1	2	3.9	2
3.5	3	4.2	3
2.1	0	4.8	4
1.9	0	5.7	9
1.5	4	5.0	7

1-10 of 20 rows

Previous 1 2 Next

Hide

worms[,sapply(worms,is.factor)]

Field.Name	Vegetation
<fctr>	<fctr>
Nashs.Field	Grassland
Silwood.Bottom	Arable
Nursery.Field	Grassland
Rush.Meadow	Meadow

Field.Name<fctr>	Vegetation<fctr>
Gunness.Thicket	Scrub
Oak.Mead	Grassland
Church.Field	Grassland
Ashurst	Arable
The.Orchard	Orchard
Rookery.Slope	Grassland
1-10 of 20 rows	
Previous12Next	

Hide

worms[-(6:15),]

	Field.Name<fctr>	Area<dbl>	Slope<int>	Vegetation<fctr>	Soil.pH<dbl>	Damp<lg>	Worm.density<int>
1	Nashs.Field	3.6	11	Grassland	4.1	FALSE	4
2	Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
3	Nursery.Field	2.8	3	Grassland	4.3	FALSE	2
4	Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
5	Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6
16	Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
17	Cheapside	2.2	8	Scrub	4.7	TRUE	4
18	Pound.Hill	4.4	2	Arable	4.5	FALSE	5
19	Gravel.Pit	2.9	1	Grassland	3.5	FALSE	1
20	Farm.Wood	0.8	10	Scrub	5.1	TRUE	3
1-10 of 10 rows							

Hide

worms[!(Vegetation=="Grassland"),]

	Field.Name<fctr>	Area<dbl>	Slope<int>	Vegetation<fctr>	Soil.pH<dbl>	Damp<lg>	Worm.density<int>
2	Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
4	Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5

	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lg>	Worm.density <int>
5	Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6
8	Ashurst	2.1	0	Arable	4.8	FALSE	4
9	The.Orchard	1.9	0	Orchard	5.7	FALSE	9
11	Garden.Wood	2.9	10	Scrub	5.2	FALSE	8
15	Pond.Field	4.1	0	Meadow	5.0	TRUE	6
16	Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
17	Cheapside	2.2	8	Scrub	4.7	TRUE	4
18	Pound.Hill	4.4	2	Arable	4.5	FALSE	5
1-10 of 11 rows							Previous 1 2 Next

Hide

worms[-which(Damp==F),]

	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lg>	Worm.density <int>
4	Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
10	Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
15	Pond.Field	4.1	0	Meadow	5.0	TRUE	6
16	Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
17	Cheapside	2.2	8	Scrub	4.7	TRUE	4
20	Farm.Wood	0.8	10	Scrub	5.1	TRUE	3
6 rows							

Hide

worms[!Damp==F,]

	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lg>	Worm.density <int>
4	Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
10	Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
15	Pond.Field	4.1	0	Meadow	5.0	TRUE	6
16	Water.Meadow	3.9	0	Meadow	4.9	TRUE	8

Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
<fctr>	<dbl>	<int>	<fctr>	<dbl>	<lgl>	<int>
17 Cheapside	2.2	8	Scrub	4.7	TRUE	4
20 Farm.Wood	0.8	10	Scrub	5.1	TRUE	3

6 rows

Hide

```
worms[Damp==T, ]
```

Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
<fctr>	<dbl>	<int>	<fctr>	<dbl>	<lgl>	<int>
4 Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
10 Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
15 Pond.Field	4.1	0	Meadow	5.0	TRUE	6
16 Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
17 Cheapside	2.2	8	Scrub	4.7	TRUE	4
20 Farm.Wood	0.8	10	Scrub	5.1	TRUE	3

6 rows

Section 4.5

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
data <- read.table("worms.missing.txt",header=F)
data
```

V1	V2	V3	V4	V5	V6	V7
<fctr>	<fctr>	<fctr>	<fctr>	<fctr>	<fctr>	<fctr>
Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
Nashs.Field	3.6	11	Grassland	4.1	F	4

V1 <fctr>	V2 <fctr>	V3 <fctr>	V4 <fctr>	V5 <fctr>	V6 <fctr>	V7 <fctr>
Silwood.Bottom	5.1	NA	Arable	5.2	F	7
Nursery.Field	2.8	3	Grassland	4.3	F	2
Rush.Meadow	2.4	5	Meadow	4.9	T	5
Gunness.Thicket	3.8	0	Scrub	4.2	F	6
Oak.Mead	3.1	2	Grassland	3.9	F	2
Church.Field	3.5	3	Grassland	NA	NA	NA
Ashurst	2.1	0	Arable	4.8	F	4
The.Orchard	1.9	0	Orchard	5.7	F	9
1-10 of 21 rows					Previous	1 2 3 Next

Hide

```
na.omit(data)
```

V1 <fctr>	V2 <fctr>	V3 <fctr>	V4 <fctr>	V5 <fctr>	V6 <fctr>	V7 <fctr>
1 Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
2 Nashs.Field	3.6	11	Grassland	4.1	F	4
4 Nursery.Field	2.8	3	Grassland	4.3	F	2
5 Rush.Meadow	2.4	5	Meadow	4.9	T	5
6 Gunness.Thicket	3.8	0	Scrub	4.2	F	6
7 Oak.Mead	3.1	2	Grassland	3.9	F	2
9 Ashurst	2.1	0	Arable	4.8	F	4
10 The.Orchard	1.9	0	Orchard	5.7	F	9
11 Rookery.Slope	1.5	4	Grassland	5	T	7
12 Garden.Wood	2.9	10	Scrub	5.2	F	8
1-10 of 18 rows					Previous	1 2 Next

Hide

```
new.frame <- na.exclude(data)
```

4.5.1 Replacing NAs with zeros

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

```
data <- read.table("worms.missing.txt",header=F)
data
```

V1 <fctr>	V2 <fctr>	V3 <fctr>	V4 <fctr>	V5 <fctr>	V6 <fctr>	V7 <fctr>
Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
Nashs.Field	3.6	11	Grassland	4.1	F	4
Silwood.Bottom	5.1	NA	Arable	5.2	F	7
Nursery.Field	2.8	3	Grassland	4.3	F	2
Rush.Meadow	2.4	5	Meadow	4.9	T	5
Gunness.Thicket	3.8	0	Scrub	4.2	F	6
Oak.Mead	3.1	2	Grassland	3.9	F	2
Church.Field	3.5	3	Grassland	NA	NA	NA
Ashurst	2.1	0	Arable	4.8	F	4
The.Orchard	1.9	0	Orchard	5.7	F	9
1-10 of 21 rows					Previous	1 2 3 Next

```
na.omit(data)
```

V1 <fctr>	V2 <fctr>	V3 <fctr>	V4 <fctr>	V5 <fctr>	V6 <fctr>	V7 <fctr>
1 Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
2 Nashs.Field	3.6	11	Grassland	4.1	F	4
4 Nursery.Field	2.8	3	Grassland	4.3	F	2
5 Rush.Meadow	2.4	5	Meadow	4.9	T	5
6 Gunness.Thicket	3.8	0	Scrub	4.2	F	6

V1	V2	V3	V4	V5	V6	V7
<fctr>	<fctr>	<fctr>	<fctr>	<fctr>	<fctr>	<fctr>
7 Oak.Mead	3.1	2	Grassland	3.9	F	2
9 Ashurst	2.1	0	Arable	4.8	F	4
10 The.Orchard	1.9	0	Orchard	5.7	F	9
11 Rookery.Slope	1.5	4	Grassland	5	T	7
12 Garden.Wood	2.9	10	Scrub	5.2	F	8
1-10 of 18 rows					Previous	1 2 Next

Hide

```
new.frame <- na.exclude(data)
data[is.na(data)]<-0
```

```
invalid factor level, NA generatedinvalid factor level, NA generatedinvalid factor level, NA generated
```

Section 4.6

Hide

```
new <- worms[rev(order(Worm.density)),]
new[!duplicated(new$Vegetation),]
```

Field.Name	Area	Slope	Vegetation	Soil.pH	Damp	Worm.density
<fctr>	<dbl>	<int>	<fctr>	<dbl>	<lgl>	<int>
9 The.Orchard	1.9	0	Orchard	5.7	FALSE	9
16 Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
11 Garden.Wood	2.9	10	Scrub	5.2	FALSE	8
10 Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
2 Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
5 rows						

Section 4.7

Hide

```
worms[order(Vegetation,-Worm.density),]
```


	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
2	Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
18	Pound.Hill	4.4	2	Arable	4.5	FALSE	5
8	Ashurst	2.1	0	Arable	4.8	FALSE	4
10	Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
1	Nashs.Field	3.6	11	Grassland	4.1	FALSE	4
7	Church.Field	3.5	3	Grassland	4.2	FALSE	3
3	Nursery.Field	2.8	3	Grassland	4.3	FALSE	2
6	Oak.Mead	3.1	2	Grassland	3.9	FALSE	2
13	South.Gravel	3.7	2	Grassland	4.0	FALSE	2
12	North.Gravel	3.3	1	Grassland	4.1	FALSE	1
1-10 of 20 rows						Previous	1 2 Next

Hide

```
worms[order(-rank(Vegetation), -Worm.density),]
```

	Field.Name <fctr>	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
11	Garden.Wood	2.9	10	Scrub	5.2	FALSE	8
5	Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6
17	Cheapside	2.2	8	Scrub	4.7	TRUE	4
20	Farm.Wood	0.8	10	Scrub	5.1	TRUE	3
9	The.Orchard	1.9	0	Orchard	5.7	FALSE	9
16	Water.Meadow	3.9	0	Meadow	4.9	TRUE	8
15	Pond.Field	4.1	0	Meadow	5.0	TRUE	6
4	Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
10	Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
1	Nashs.Field	3.6	11	Grassland	4.1	FALSE	4
1-10 of 20 rows						Previous	1 2 Next

Hide

```
names(worms)
```

```
[1] "Field.Name"  "Area"        "Slope"       "Vegetation"  "Soil.pH"     "Damp"        "Worm.density"
```

Hide

```
grep("S",names(worms))
```

```
[1] 3 5
```

Hide

```
worms[,grep("S",names(worms))]
```

	Slope <int>	Soil.pH <dbl>
	11	4.1
	2	5.2
	3	4.3
	5	4.9
	0	4.2
	2	3.9
	3	4.2
	0	4.8
	0	5.7
	4	5.0

1-10 of 20 rows

Previous12Next

Hide

```
NA
```

Section 4.8

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
worms2 <- read.table("worms.txt",header=T,row.names=1)
worms2
```

	Area <dbl>	Slope <int>	Vegetation <fctr>	Soil.pH <dbl>	Damp <lgl>	Worm.density <int>
Nashs.Field	3.6	11	Grassland	4.1	FALSE	4
Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7
Nursery.Field	2.8	3	Grassland	4.3	FALSE	2
Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5
Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6
Oak.Mead	3.1	2	Grassland	3.9	FALSE	2
Church.Field	3.5	3	Grassland	4.2	FALSE	3
Ashurst	2.1	0	Arable	4.8	FALSE	4
The.Orchard	1.9	0	Orchard	5.7	FALSE	9
Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7
1-10 of 20 rows					Previous	1 2 Next

Section 4.9

Hide

```
x <- runif(10)
y <- letters[1:10]
z <- sample(c(rep(T,5),rep(F,5)))

new <- data.frame(y,z,x)
new
```

y <fctr>	z <lgl>	x <dbl>
a	TRUE	0.1466354
b	TRUE	0.5167331
c	FALSE	0.8616611
d	TRUE	0.5357124
e	FALSE	0.5527880
f	FALSE	0.1066144

y <fctr>	z <lgl>	x <dbl>
g	TRUE	0.1170416
h	TRUE	0.5955476
i	FALSE	0.7235653
j	FALSE	0.2950741
1-10 of 10 rows		

Hide

```
y <- rpois(1500,1.5)
table(y)
```

```
y
  0   1   2   3   4   5   6
328 495 390 190  74  22   1
```

Hide

```
short<-as.data.frame(table(y))
short
```

y <fctr>	Freq <int>
0	328
1	495
2	390
3	190
4	74
5	22
6	1
7 rows	

Hide

```
index<-rep(1:8,short$Freq)
```

```
Error in rep(1:8, short$Freq) : invalid 'times' argument
```

Section 4.10

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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[Hide](#)

```
dups <- read.table("dups.txt",header=T)
dups
```

	cow <int>	dog <int>	cat <int>	bat <int>
	1	2	3	1
	1	2	2	1
	3	2	1	1
	4	4	2	1
	3	2	1	1
	6	1	2	5
	1	2	3	2

7 rows

[Hide](#)

```
unique(dups)
```

	cow <int>	dog <int>	cat <int>	bat <int>
1	1	2	3	1
2	1	2	2	1
3	3	2	1	1
4	4	4	2	1
6	6	1	2	5
7	1	2	3	2

6 rows

Hide

```
dups[duplicated(dups),]
```

	cow <int>	dog <int>	cat <int>	bat <int>
5	3	2	1	1
1 row				

Hide

NA

Section 4.11

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
nums <- read.table("sortdata.txt",header=T)
attach(nums)
head(nums)
```

	name <fctr>	date <fctr>	response <dbl>	treatment <fctr>
1	albert	25/08/2003	0.05963704	A
2	ann	21/05/2003	1.46555993	A
3	john	12/10/2003	1.59406539	B
4	ian	02/12/2003	2.09505949	A
5	michael	18/10/2003	2.38330748	B
6	ann	02/07/2003	2.86983693	B
6 rows				

Hide

```
nums[order(date),]
```

	name <fctr>	date <fctr>	response <dbl>	treatment <fctr>
53	rachel	01/08/2003	32.98792196	B
65	albert	02/06/2003	38.41979568	A
6	ann	02/07/2003	2.86983693	B
10	cecily	02/11/2003	6.81467570	A
4	ian	02/12/2003	2.09505949	A
29	michael	03/05/2003	15.59890900	B
67	william	03/09/2003	38.95014474	A
26	heather	03/10/2003	12.79110099	B
36	elizabeth	04/08/2003	21.46862324	B
8	james	05/06/2003	4.90041370	A
1-10 of 76 rows			Previous	1 2 3 4 5 6 ... 8 Next

[Hide](#)

```
dates <- strptime(date,format="%d/%m/%Y")
dates
```

```
[1] "2003-08-25 EDT" "2003-05-21 EDT" "2003-10-12 EDT" "2003-12-02 EST" "2003-10-18 EDT" "2003-07-02 EDT" "2003-09-27 EDT"
[8] "2003-06-05 EDT" "2003-06-11 EDT" "2003-11-02 EST" "2003-09-24 EDT" "2003-11-26 EST" "2003-11-08 EST" "2003-07-11 EDT"
[15] "2003-09-12 EDT" "2003-05-27 EDT" "2003-09-06 EDT" "2003-09-30 EDT" "2003-05-30 EDT" "2003-07-20 EDT" "2003-07-29 EDT"
[22] "2003-10-15 EDT" "2003-09-18 EDT" "2003-04-27 EDT" "2003-11-17 EST" "2003-10-03 EDT" "2003-11-23 EST" "2003-11-11 EST"
[29] "2003-05-03 EDT" "2003-11-20 EST" "2003-10-30 EST" "2003-09-15 EDT" "2003-04-30 EDT" "2003-06-08 EDT" "2003-05-18 EDT"
[36] "2003-08-04 EDT" "2003-08-13 EDT" "2003-08-07 EDT" "2003-10-21 EDT" "2003-11-29 EST" "2003-06-17 EDT" "2003-08-19 EDT"
[43] "2003-10-27 EST" "2003-10-06 EDT" "2003-11-05 EST" "2003-07-05 EDT" "2003-07-26 EDT" "2003-06-20 EDT" "2003-04-21 EDT"
[50] "2003-05-09 EDT" "2003-07-17 EDT" "2003-08-31 EDT" "2003-08-01 EDT" "2003-10-09 EDT" "2003-07-23 EDT" "2003-09-21 EDT"
[57] "2003-08-28 EDT" "2003-06-29 EDT" "2003-07-08 EDT" "2003-08-22 EDT" "2003-06-26 EDT" "2003-08-10 EDT" "2003-04-24 EDT"
[64] "2003-10-24 EDT" "2003-06-02 EDT" "2003-09-09 EDT" "2003-09-03 EDT" "2003-07-14 EDT" "2003-05-12 EDT" "2003-06-14 EDT"
[71] "2003-05-06 EDT" "2003-05-15 EDT" "2003-05-24 EDT" "2003-08-16 EDT" "2003-11-14 EST" "2003-06-23 EDT"
```

Hide

```
nums <- cbind(nums,dates)
nums[order(dates),]
```

	name <fctr>	date <fctr>	response <dbl>	treatment <fctr>	dates <S3: POSIXct>
49	albert	21/04/2003	30.66632632	A	2003-04-21
63	james	24/04/2003	37.04140266	A	2003-04-24
24	john	27/04/2003	12.70257306	A	2003-04-27
33	william	30/04/2003	18.05707279	B	2003-04-30
29	michael	03/05/2003	15.59890900	B	2003-05-03
71	ian	06/05/2003	39.97237868	A	2003-05-06
50	rachel	09/05/2003	30.81807436	B	2003-05-09
69	elizabeth	12/05/2003	39.39536726	B	2003-05-12
72	rose	15/05/2003	39.98892034	A	2003-05-15
35	cecily	18/05/2003	21.27373776	B	2003-05-18
1-10 of 76 rows			Previous	1 2 3 4 5 6 ... 8	Next

Hide

NA

Section 4.12

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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Hide

```
unique(worms$Vegetation)
```

```
[1] Grassland Arable Meadow Scrub Orchard
Levels: Arable Grassland Meadow Orchard Scrub
```

Hide


```
herbicides <- read.table("herbicides.txt",header=T)
herbicides
```

Type <fctr>	Herbicide <fctr>
Woodland	Fusilade
Conifer	Weedwipe
Arable	Twinspan
Hill	Weedwipe
Bracken	Fusilade
Scrub	Weedwipe
Grassland	Allclear
Chalk	Vanquish
Meadow	Propinol
Lawn	Vanquish

1-10 of 12 rows

Previous12Next

Hide

```
herbicides$Herbicide[match(worms$Vegetation,herbicides$Type)]
```

```
[1] Allclear Twinspan Allclear Propinol Weedwipe Allclear Allclear Twinspan Fusilade Allclear Weedwipe Allclear Allclear Allclear
[15] Propinol Propinol Weedwipe Twinspan Allclear Weedwipe
Levels: Allclear Fusilade Propinol Twinspan Vanquish Weedwipe
```

Hide

```
worms$hb <- herbicides$Herbicide[match(worms$Vegetation,herbicides$Type)]

recs <- data.frame(
  worms,hb=herbicides$Herbicide[match(worms$Vegetation,herbicides$Type)])
recs
```

Field.Name <fctr>	A... <dbl>	SI... <int>	Vegetation <fctr>	Soil.pH <dbl>	Da... <lgf>	Worm.density <int>	hb <fctr>	hb.1 <fctr>
Nashs.Field	3.6	11	Grassland	4.1	FALSE	4	Allclear	Allclear
Silwood.Bottom	5.1	2	Arable	5.2	FALSE	7	Twinspan	Twinspan
Nursery.Field	2.8	3	Grassland	4.3	FALSE	2	Allclear	Allclear

Field.Name <fctr>	A... <dbl>	SI... <int>	Vegetation <fctr>	Soil.pH <dbl>	Da... <lgl>	Worm.density <int>	hb <fctr>	hb.1 <fctr>
Rush.Meadow	2.4	5	Meadow	4.9	TRUE	5	Propinol	Propinol
Gunness.Thicket	3.8	0	Scrub	4.2	FALSE	6	Weedwipe	Weedwipe
Oak.Mead	3.1	2	Grassland	3.9	FALSE	2	Allclear	Allclear
Church.Field	3.5	3	Grassland	4.2	FALSE	3	Allclear	Allclear
Ashurst	2.1	0	Arable	4.8	FALSE	4	Twinspan	Twinspan
The.Orchard	1.9	0	Orchard	5.7	FALSE	9	Fusilade	Fusilade
Rookery.Slope	1.5	4	Grassland	5.0	TRUE	7	Allclear	Allclear
1-10 of 20 rows							Previous	1 2 Next

Hide

NA

Section 4.13

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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Hide

```
(lifeforms <- read.table("lifeforms.txt",header=T))
```

Genus <fctr>	species <fctr>	lifeform <fctr>
Acer	platanoides	tree
Acer	palmatum	tree
Ajuga	reptans	herb
Conyza	sumatrensis	annual
Lamium	album	herb
5 rows		

Hide

```
(flowering <- read.table("fltimes.txt",header=T))
```

Genus <fctr>	species <fctr>	flowering <fctr>
Acer	platanoides	May
Ajuga	reptans	June
Brassica	napus	April
Chamerion	angustifolium	July
Conyza	bilbaoana	August
Lamium	album	January

6 rows

Hide

```
merge(flowering,lifeforms)
```

Genus <fctr>	species <fctr>	flowering <fctr>	lifeform <fctr>
Acer	platanoides	May	tree
Ajuga	reptans	June	herb
Lamium	album	January	herb

3 rows

Hide

```
(both <- merge(flowering,lifeforms,all=T))
```

Genus <fctr>	species <fctr>	flowering <fctr>	lifeform <fctr>
Acer	platanoides	May	tree
Acer	palmatum	NA	tree
Ajuga	reptans	June	herb
Brassica	napus	April	NA
Chamerion	angustifolium	July	NA
Conyza	bilbaoana	August	NA

Genus <fctr>	species <fctr>	flowering <fctr>	lifeform <fctr>
Conyza	sumatrensis	NA	annual
Lamium	album	January	herb
8 rows			

Hide

```
(seeds <- read.table("seedwts.txt",header=T))
```

name1 <fctr>	name2 <fctr>	seed <dbl>
Acer	platanoides	32.0
Lamium	album	12.0
Ajuga	reptans	4.0
Chamerion	angustifolium	1.5
Conyza	bilbaoana	0.5
Brassica	napus	7.0
Acer	palmatum	21.0
Conyza	sumatrensis	0.6
8 rows		

Hide

```
merge(both,seeds,by.x=c("Genus","species"),by.y=c("name1","name2"))
```

Genus <fctr>	species <fctr>	flowering <fctr>	lifeform <fctr>	seed <dbl>
Acer	palmatum	NA	tree	21.0
Acer	platanoides	May	tree	32.0
Ajuga	reptans	June	herb	4.0
Brassica	napus	April	NA	7.0
Chamerion	angustifolium	July	NA	1.5
Conyza	bilbaoana	August	NA	0.5
Conyza	sumatrensis	NA	annual	0.6

Genus <fctr>	species <fctr>	flowering <fctr>	lifeform <fctr>	seed <dbl>
Lamium	album	January	herb	12.0

8 rows

Section 4.14

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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Hide

```
frame <- read.table("sales.txt",header=T)
frame
```

name <fctr>	spring <int>	summer <int>	autumn <int>	winter <int>
Jane.Smith	14	18	11	12
Robert.Jones	17	18	10	13
Dick.Rogers	12	16	9	14
William.Edwards	15	14	11	10
Janet.Jones	11	17	11	16

5 rows

Hide

```
people <- rowMeans(frame[,2:5])
people <- people-mean(people)
people
```

```
[1] 0.30 1.05 -0.70 -0.95 0.30
```

Hide

```
(new.frame <- cbind(frame,people))
```

name <fctr>	spring <int>	summer <int>	autumn <int>	winter <int>	people <dbl>
Jane.Smith	14	18	11	12	0.30
Robert.Jones	17	18	10	13	1.05
Dick.Rogers	12	16	9	14	-0.70
William.Edwards	15	14	11	10	-0.95
Janet.Jones	11	17	11	16	0.30

5 rows

Hide

```
seasons <- colMeans(frame[,2:5])
seasons <- seasons-mean(seasons)
seasons
```

```
spring summer autumn winter
0.35    3.15   -3.05   -0.45
```

Hide

```
new.row <- new.frame[1,]
new.row[1] <- "seasonal effects"
new.row[2:5] <- seasons
new.row[6] <- 0
new.row
```

name <chr>	spring <dbl>	summer <dbl>	autumn <dbl>	winter <dbl>	people <dbl>
1 seasonal effects	0.35	3.15	-3.05	-0.45	0

1 row

Hide

```
(new.frame <- rbind(new.frame,new.row))
```

name <fctr>	spring <dbl>	summer <dbl>	autumn <dbl>	winter <dbl>	people <dbl>
Jane.Smith	14.00	18.00	11.00	12.00	0.30
Robert.Jones	17.00	18.00	10.00	13.00	1.05
Dick.Rogers	12.00	16.00	9.00	14.00	-0.70
William.Edwards	15.00	14.00	11.00	10.00	-0.95

name <fctr>	spring <dbl>	summer <dbl>	autumn <dbl>	winter <dbl>	people <dbl>
Janet.Jones	11.00	17.00	11.00	16.00	0.30
seasonal effects	0.35	3.15	-3.05	-0.45	0.00

6 rows

Hide

```
gm <- mean(unlist(new.frame[1:5,2:5]))
gm <- rep(gm,4)
new.frame[1:5,2:5] <- sweep(new.frame[1:5,2:5],2,gm)
new.frame
```

name <fctr>	spring <dbl>	summer <dbl>	autumn <dbl>	winter <dbl>	people <dbl>
Jane.Smith	0.55	4.55	-2.45	-1.45	0.30
Robert.Jones	3.55	4.55	-3.45	-0.45	1.05
Dick.Rogers	-1.45	2.55	-4.45	0.55	-0.70
William.Edwards	1.55	0.55	-2.45	-3.45	-0.95
Janet.Jones	-2.45	3.55	-2.45	2.55	0.30
seasonal effects	0.35	3.15	-3.05	-0.45	0.00

6 rows

Hide

```
new.frame[6,6] <- gm[1]
new.frame
```

name <fctr>	spring <dbl>	summer <dbl>	autumn <dbl>	winter <dbl>	people <dbl>
Jane.Smith	0.55	4.55	-2.45	-1.45	0.30
Robert.Jones	3.55	4.55	-3.45	-0.45	1.05
Dick.Rogers	-1.45	2.55	-4.45	0.55	-0.70
William.Edwards	1.55	0.55	-2.45	-3.45	-0.95
Janet.Jones	-2.45	3.55	-2.45	2.55	0.30
seasonal effects	0.35	3.15	-3.05	-0.45	13.45

6 rows

Hide

NA

Section 4.15

Hide

```
aggregate(worms[,c(2,3,5,7)],by=list(veg=Vegetation),mean)
```

veg <fctr>	Area <dbl>	Slope <dbl>	Soil.pH <dbl>	Worm.density <dbl>
Arable	3.866667	1.333333	4.833333	5.333333
Grassland	2.911111	3.666667	4.100000	2.444444
Meadow	3.466667	1.666667	4.933333	6.333333
Orchard	1.900000	0.000000	5.700000	9.000000
Scrub	2.425000	7.000000	4.800000	5.250000
5 rows				

Hide

```
aggregate(worms[,c(2,3,5,7)],by=list(veg=Vegetation,d=Damp),mean)
```

veg <fctr>	d <lgl>	Area <dbl>	Slope <dbl>	Soil.pH <dbl>	Worm.density <dbl>
Arable	FALSE	3.866667	1.333333	4.833333	5.333333
Grassland	FALSE	3.087500	3.625000	3.987500	1.875000
Orchard	FALSE	1.900000	0.000000	5.700000	9.000000
Scrub	FALSE	3.350000	5.000000	4.700000	7.000000
Grassland	TRUE	1.500000	4.000000	5.000000	7.000000
Meadow	TRUE	3.466667	1.666667	4.933333	6.333333
Scrub	TRUE	1.500000	9.000000	4.900000	3.500000
7 rows					

Hide

NA

Chapter 5

Section 5.1

None # Section 5.2

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
data1 <- read.table("scatter1.txt",header=T)

attach(data1)
names(data1)
```

```
[1] "xv" "ys"
```

Hide

```
head(data1)
```

	xv <dbl>	ys <dbl>
1	90.77212	51.75918
2	16.11536	28.95312
3	31.12350	35.50002
4	39.79581	32.69104
5	48.82297	40.50366
6	78.17519	56.58430
6 rows		

Hide

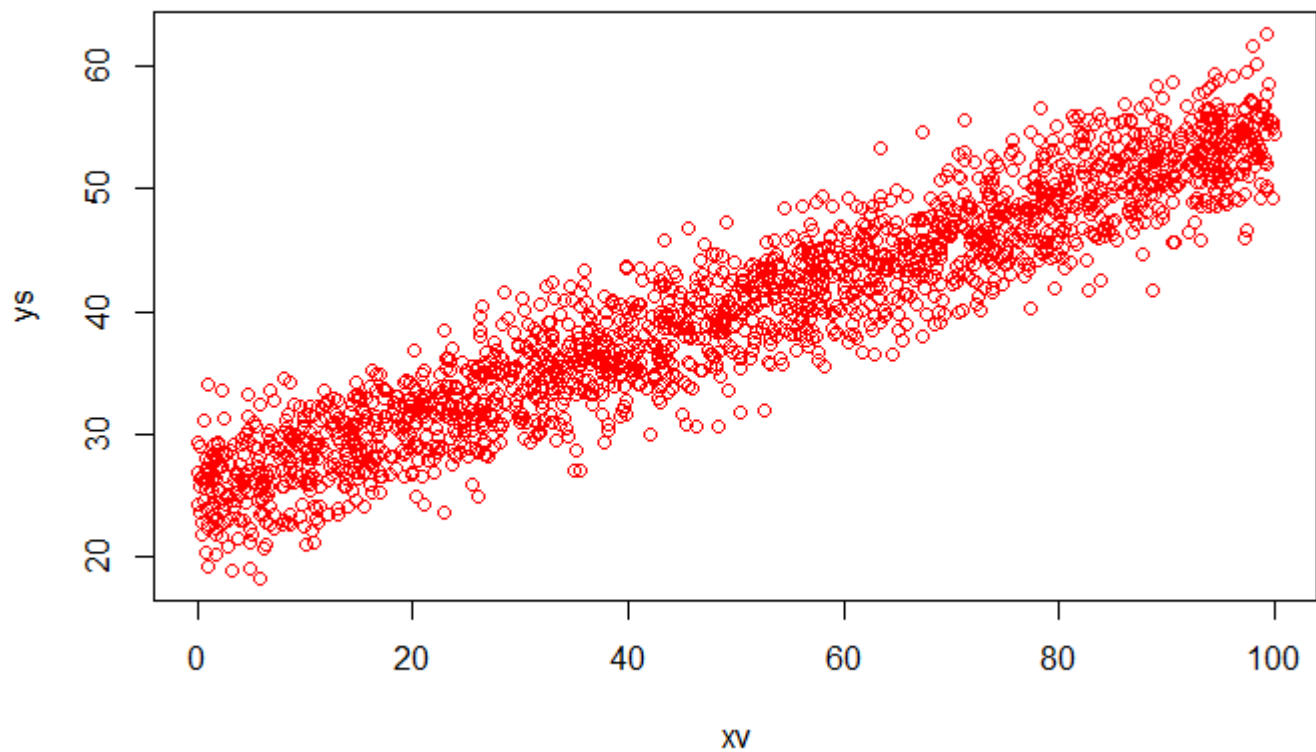
```
tail(data1)
```

	xv <dbl>	ys <dbl>
1995	17.31421000	31.50580
1996	71.92099000	46.01331

	xv <dbl>	ys <dbl>
1997	85.27439000	51.86151
1998	0.02849861	24.24000
1999	99.20837000	50.20170
2000	48.45682000	40.97587
6 rows		

[Hide](#)

```
plot(xv,ys,col="red")
```

[Hide](#)

```
plot(xv,ys,col="red",xlab="Explanatory variable",ylab="Response variable")  
abline(lm(ys~xv))
```

[Hide](#)

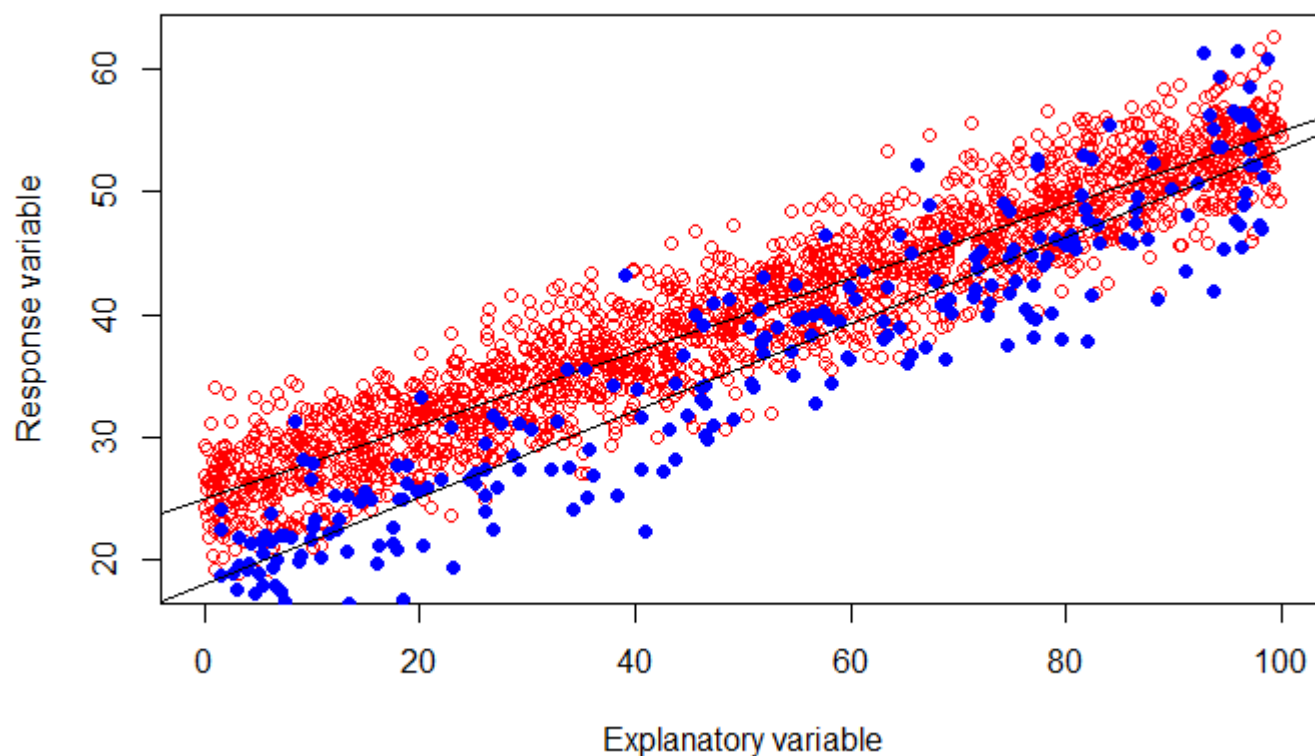
```
#data2 <- read.table("scatter2.txt",header=T)
data2 <- read.table("scatter2.txt",header=T)

attach(data2)
names(data2)
```

```
[1] "xv2" "ys2"
```

[Hide](#)

```
points(xv2,ys2,col="blue",pch=16)
abline(lm(ys2~xv2))
```


[Hide](#)

```
plot(c(xv,xv2),c(ys,ys2),xlab="Explanatory variable",
      ylab="Response variable",type="n")

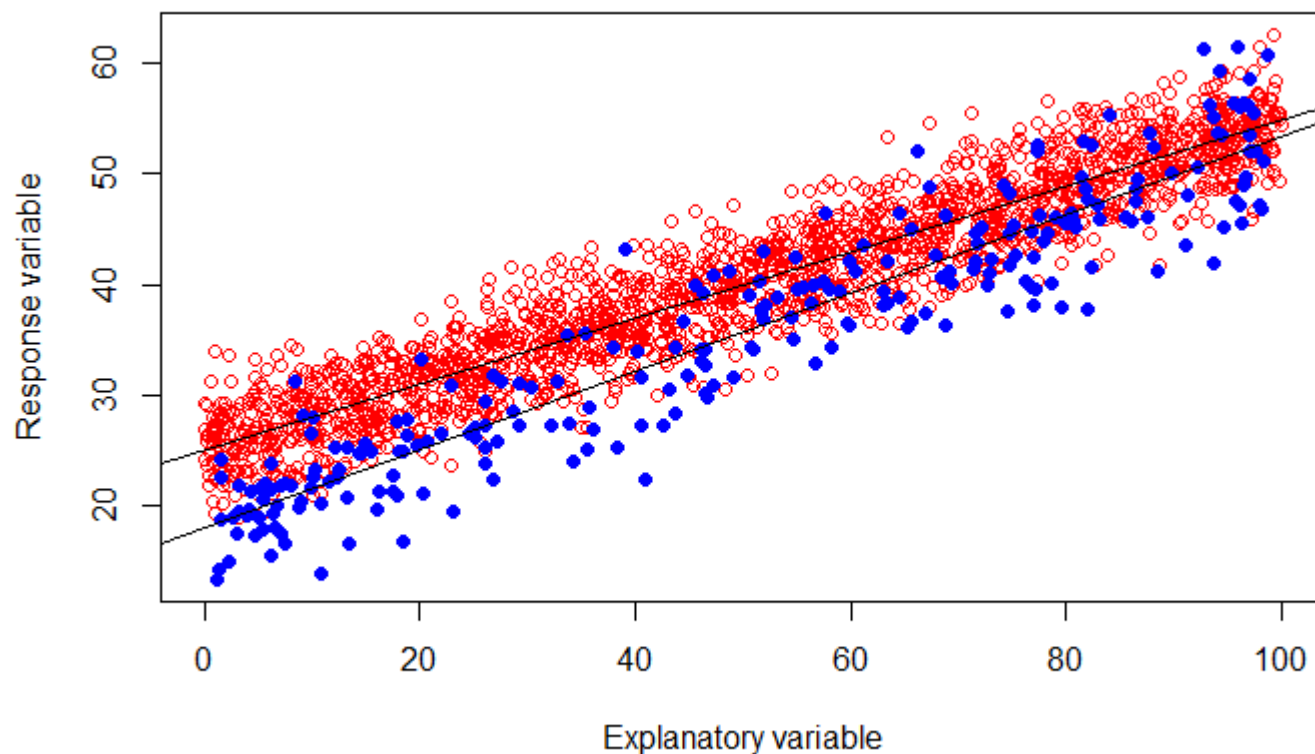
points(xv,ys,col="red")
```

[Hide](#)

```
points(xv2,ys2,col="blue",pch=16)
abline(lm(ys~xv))
```

Hide

```
abline(lm(ys2~xv2))
```



Hide

```
range(c(xv,xv2))
```

```
[1] 0.02849861 99.93262000
```

Hide

```
range(c(ys,ys2))
```

```
[1] 13.41794 62.59482
```

Hide

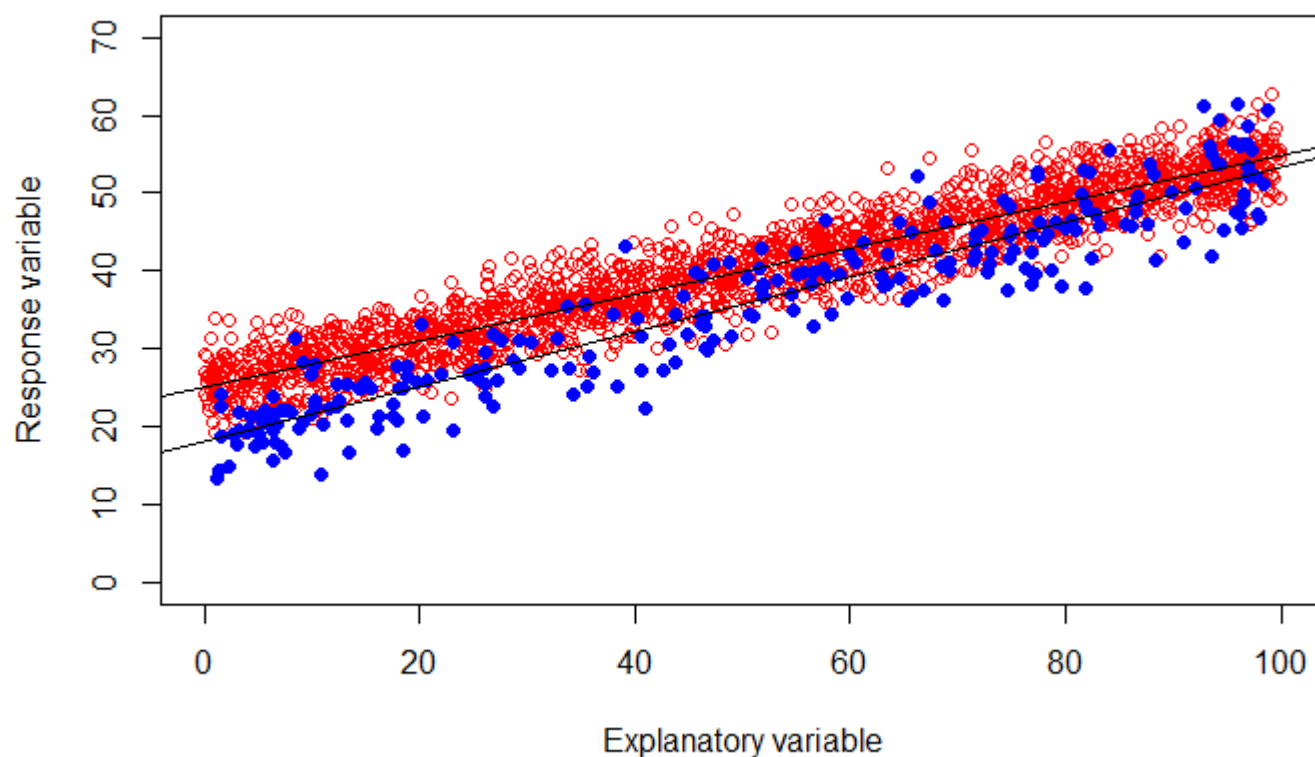
```
plot(c(xv,xv2),c(ys,ys2),xlim=c(0,100),ylim=c(0,70),
     xlab="Explanatory variable",ylab="Response variable",type="n")
points(xv,ys,col="red")
```

Hide

```
points(xv2,ys2,col="blue",pch=16)
abline(lm(ys~xv))
```

Hide

```
abline(lm(ys2~xv2))
```



Hide

```
# click the mouse button when the cursor is where you want to
# the top left of the box around the legend to be
legend(locator(1),c("treatment","control"),pch=c(1,16), col=c("red","blue"))
```

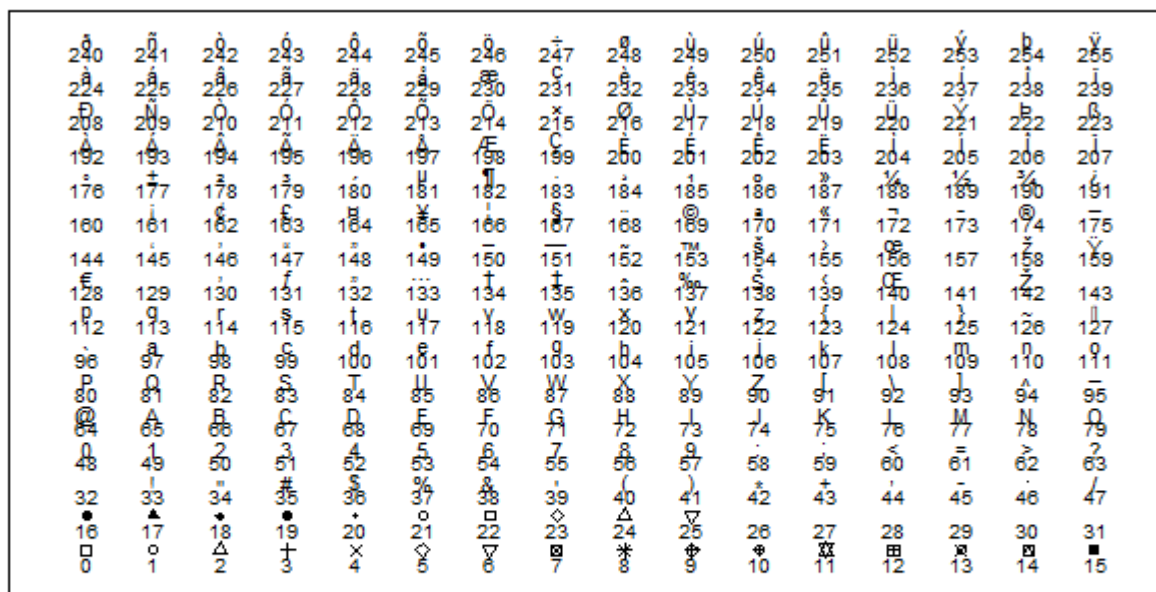
```
Error in legend(locator(1), c("treatment", "control"), pch = c(1, 16), :
invalid coordinate lengths
```

Section 5.2.1

Hide

```
plot(0:10,0:10,xlim=c(0,32),ylim=c(0,40),type="n",xaxt="n",yaxt="n",
     xlab="",ylab="")
x <- seq(1,31,2)
s <- -16
f <- -1
for (y in seq(2,40,2.5)) {
  s <- s+16
  f <- f+16
  y2 <- rep(y,16)
  points(x,y2,pch=s:f,cex=0.7)
  text(x,y-1,as.character(s:f),cex=0.6) }
```

unimplemented pch value '26'unimplemented pch value '27'unimplemented pch value '28'unimplemented pch value '29'unimplemented pch value '30'unimplemented pch value '31'



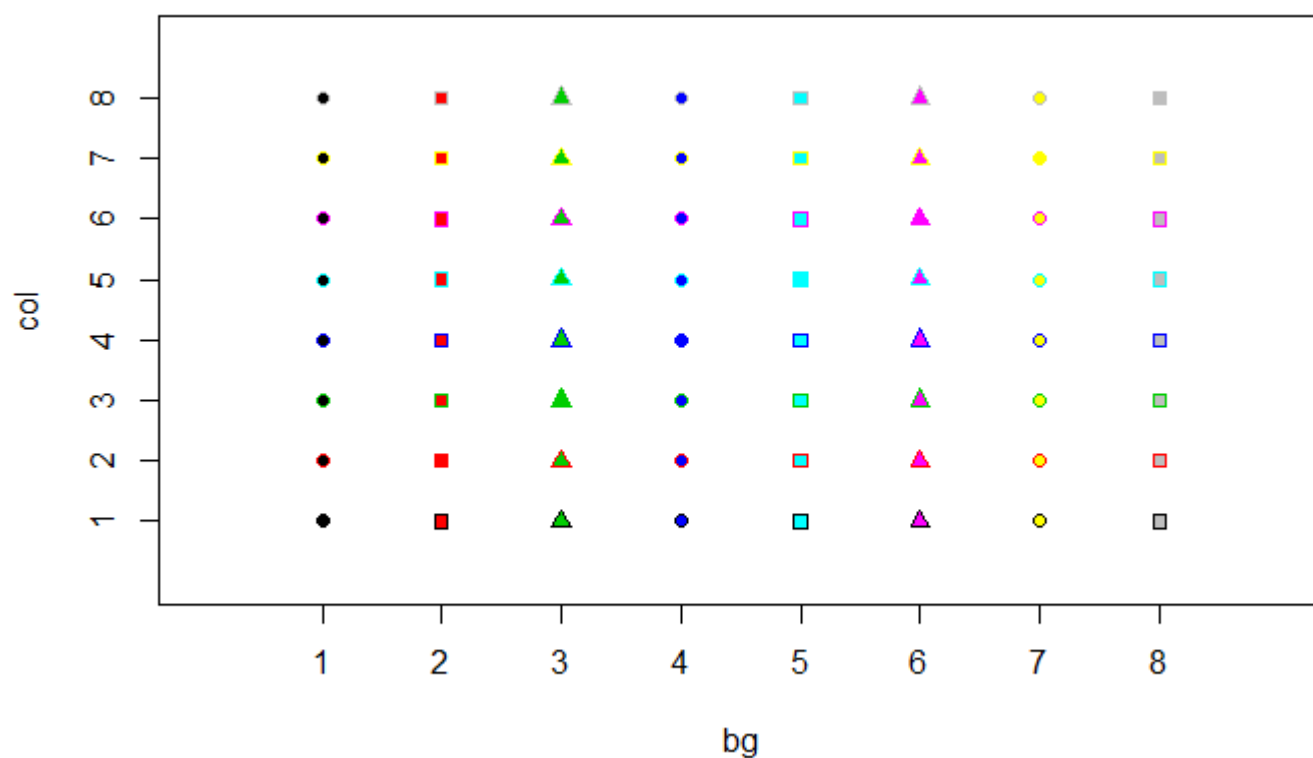
Section 5.2.2

[Hide](#)

```
plot(0:9,0:9,pch=16,type="n",xaxt="n",yaxt="n",ylab="col",xlab="bg")
axis(1,at=1:8)
```

[Hide](#)

```
axis(2,at=1:8)
for (i in 1:8) points(1:8,rep(i,8),pch=c(21,22,24),bg=1:8,col=i)
```



Section 5.2.3

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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[Hide](#)

```
map.places <- read.csv("map.places.csv",header=T)
attach(map.places)
```

The following object is masked from map.places (pos = 3):

wanted

[Hide](#)

```
names(map.places)
```

```
[1] "wanted"
```

Hide

```
map.data <- read.csv("bowens.csv",header=T)
attach(map.data)
names(map.data)
```

```
[1] "place" "east"  "north"
```

Hide

```
nn <- ifelse(north<60,north+100,north)
windows(9,7)
plot(c(20,100),c(60,110),type="n",xlab="",ylab="",xaxt="n", yaxt="n")
for (i in 1:length(wanted)){
  ii <- which(place == as.character(wanted[i]))
  text(east[ii], nn[ii], as.character(place[ii]), cex = 0.6) }
```

Section 5.2.4

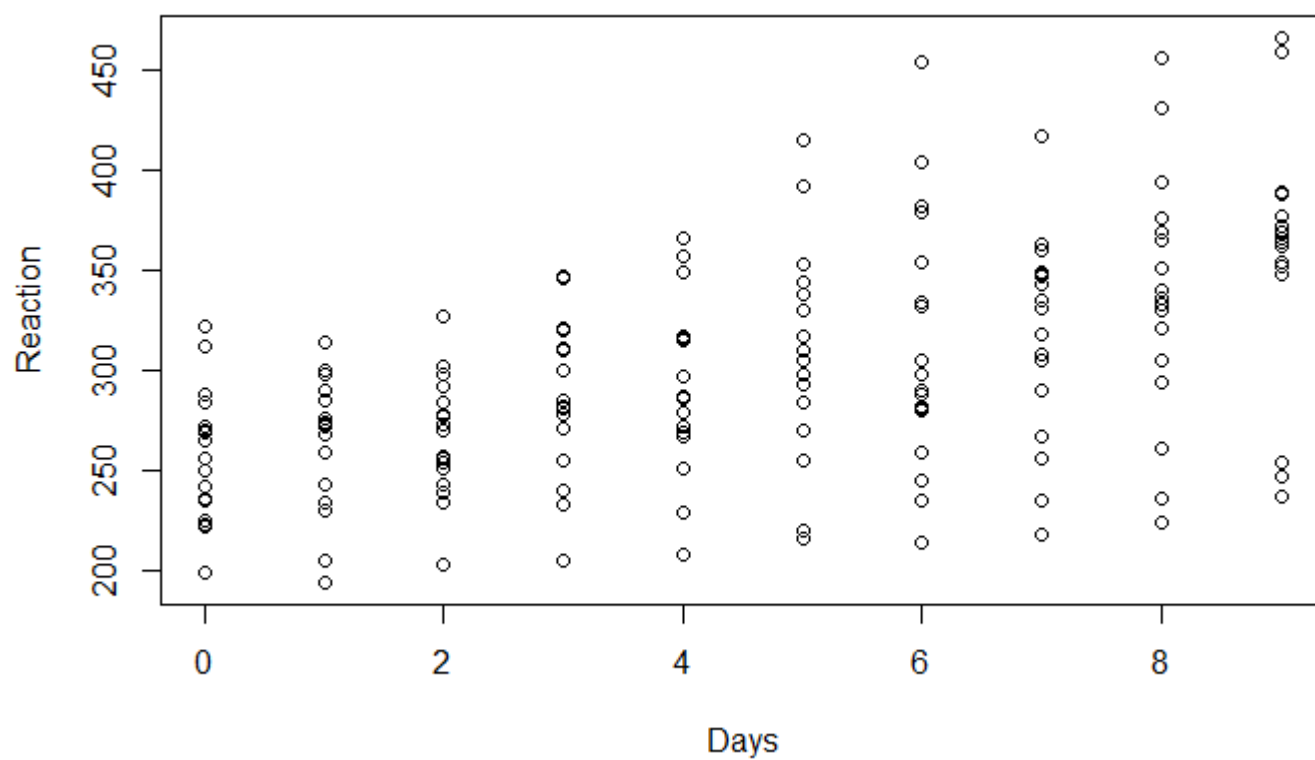
Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
data <- read.table("sleep.txt",header=T)
attach(data)
plot(Days,Reaction)
```

Hide

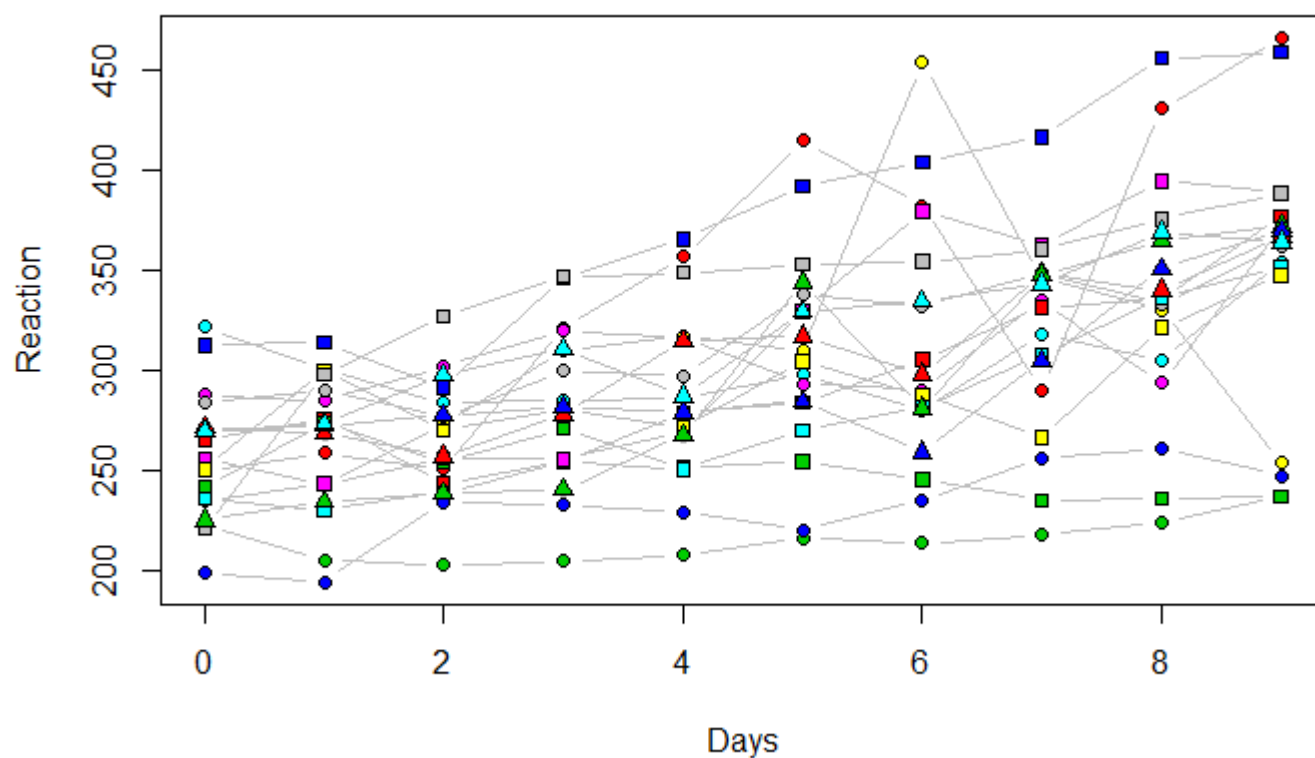
```
s <- as.numeric(factor(Subject))

plot(Days,Reaction,type="n")
for (k in 1:max(s)){
  x <- Days[s==k]
  y <- Reaction[s==k]
  lines(x,y,type="b",col="gray")
}
```

Hide

```
sym <- rep(c(21,22,24),c(7,7,4))
bcol <- c(2:8,2:8,2:5)

for (k in 1:max(s)){
  points(Days[s==k],Reaction[s==k],pch=sym[k],bg=bcol[k],col=1)
}
```



Section 5.2.5

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

[Hide](#)

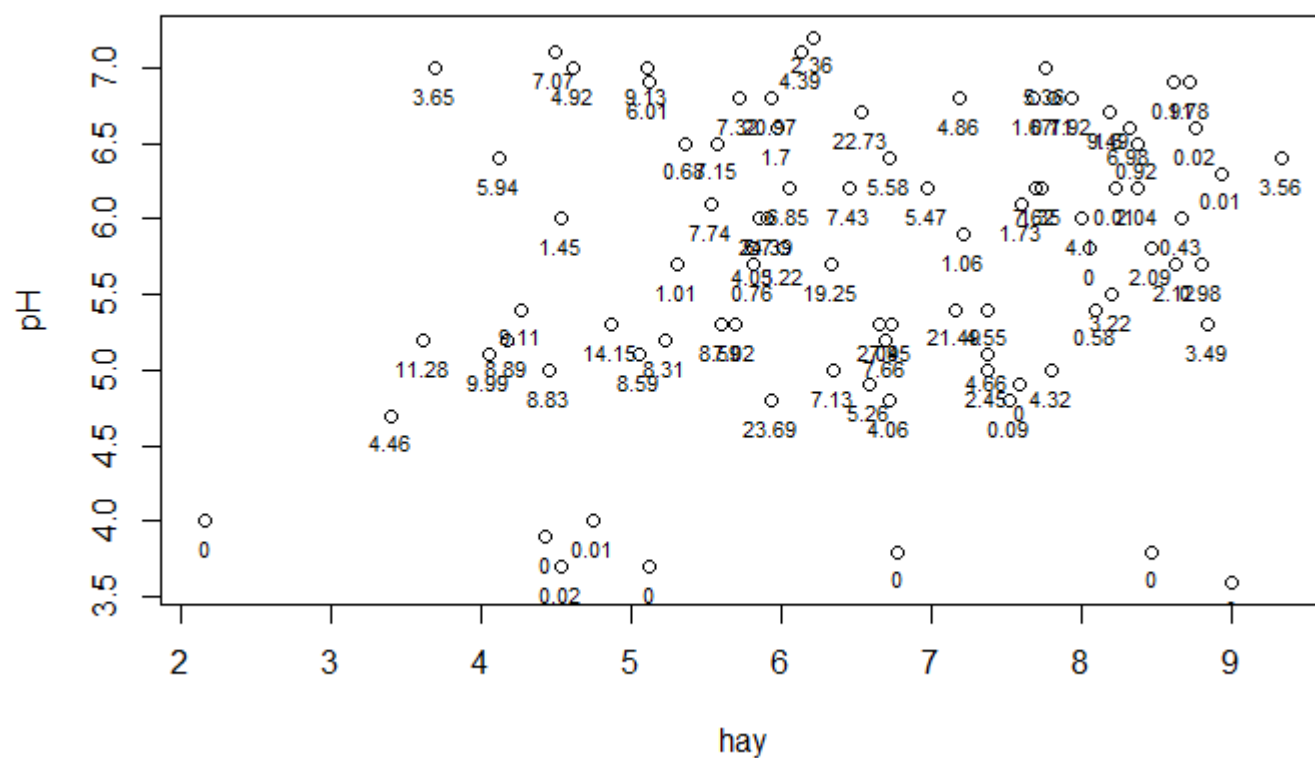
```
data <- read.table("pgr.txt",header=T)

attach(data)
names(data)
```

```
[1] "FR" "hay" "pH"
```

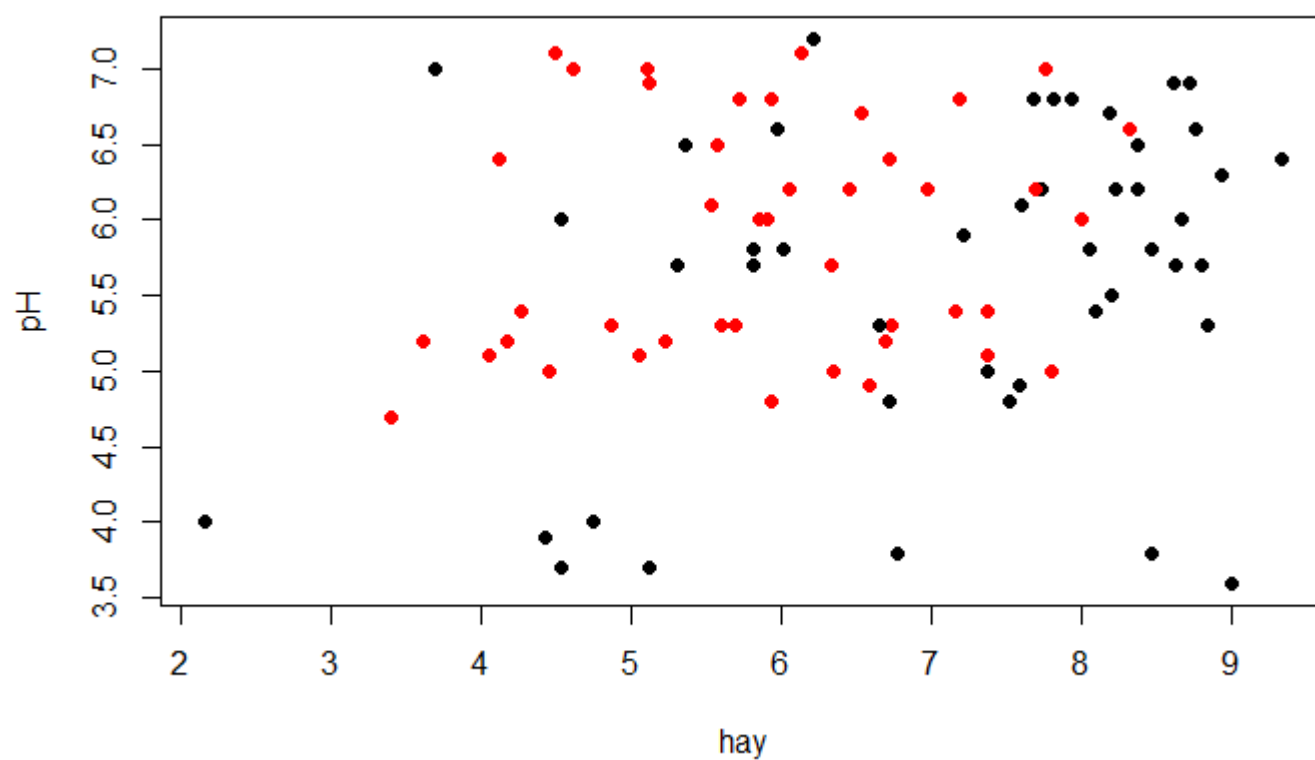
[Hide](#)

```
plot(hay,pH)
text(hay, pH, labels=round(FR, 2), pos=1, offset=0.5,cex=0.7)
```



Hide

```
plot(hay,pH,pch=16,col=ifelse(FR>median(FR),"red","black"))
```



Hide

```
legend(locator(1),c("FR>median","FR<=median"),pch=16,col=c("red","black"))
```

```
Error in legend(locator(1), c("FR>median", "FR<=median"), pch = 16, col = c("red", :  
  invalid coordinate lengths
```

Section 5.2.6

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
smooth <- read.table("smoothing.txt",header=T)  
attach(smooth)
```

The following objects are masked `_by_ .GlobalEnv:`

x, y

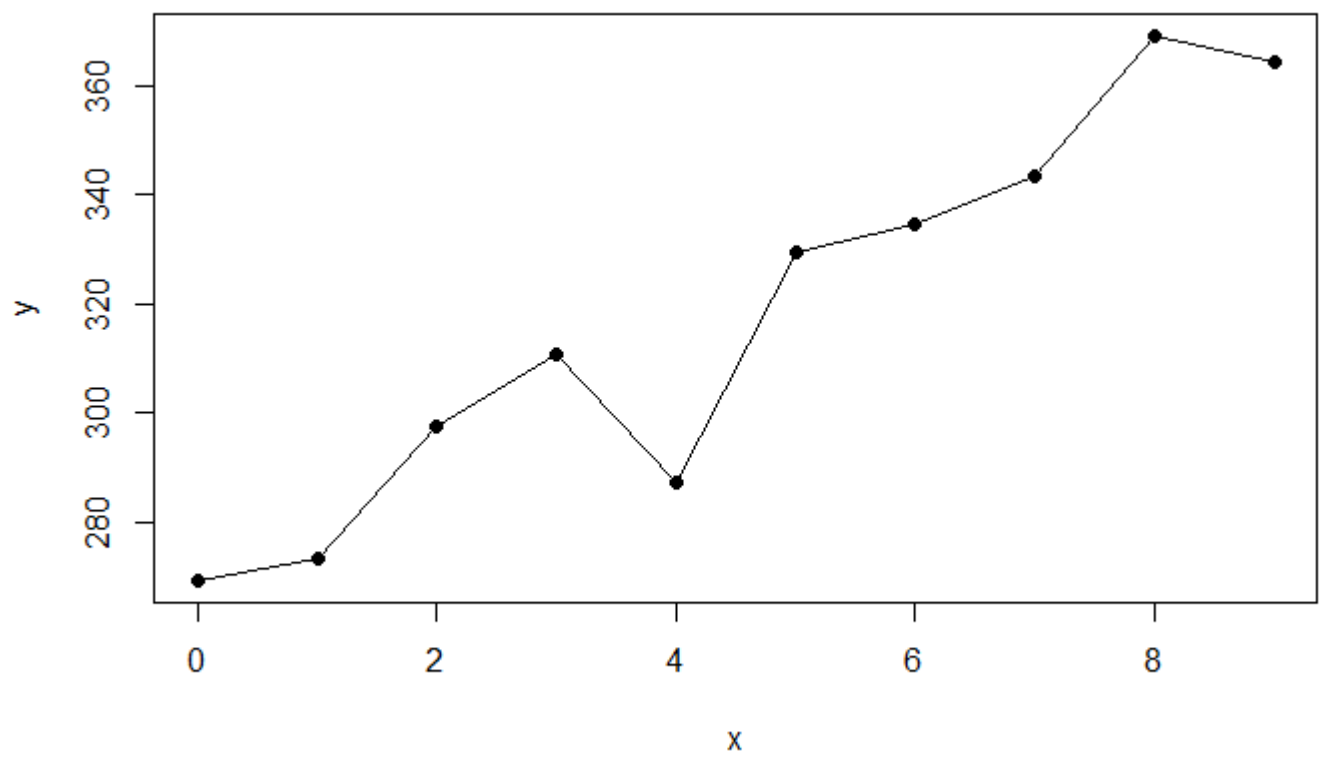
Hide

```
names(smooth)
```

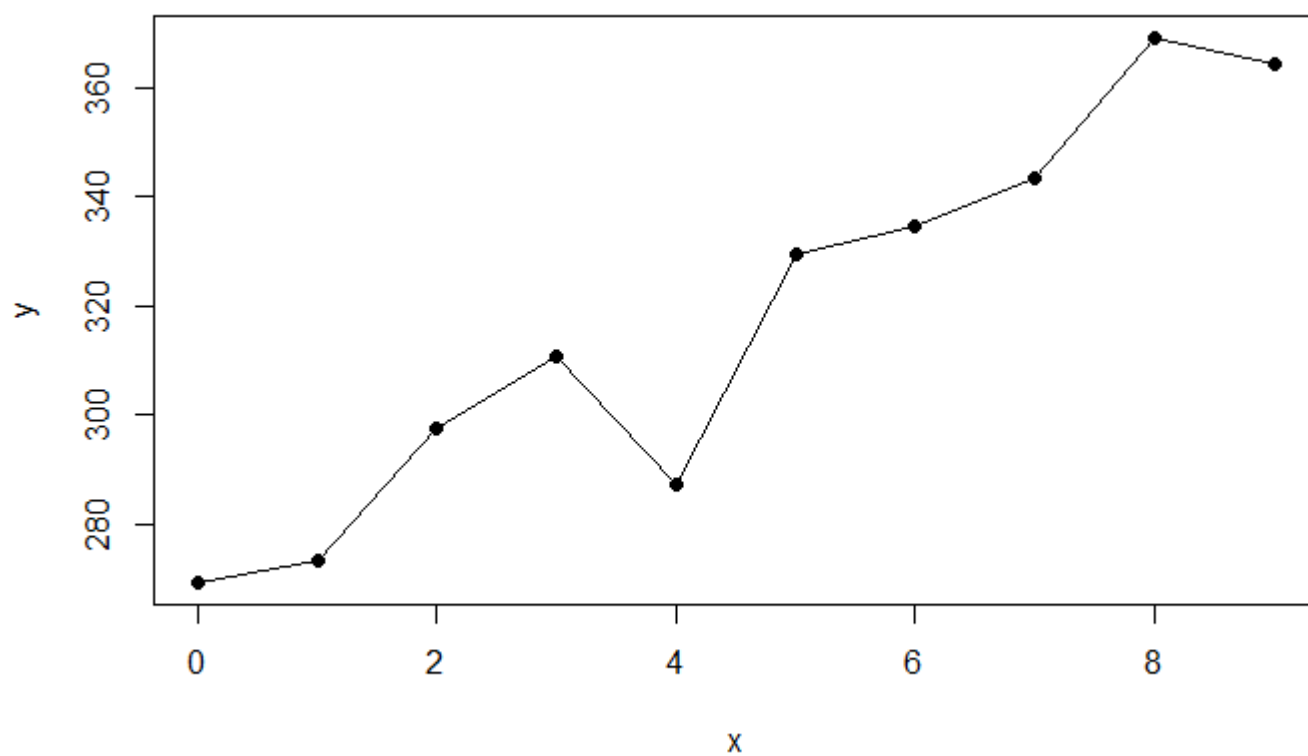
```
[1] "x" "y"
```

Hide

```
plot(x,y,pch=16)  
sequence <- order(x)  
lines(x[sequence],y[sequence])
```

[Hide](#)

```
plot(x,y,pch=16)  
lines(x,y)
```



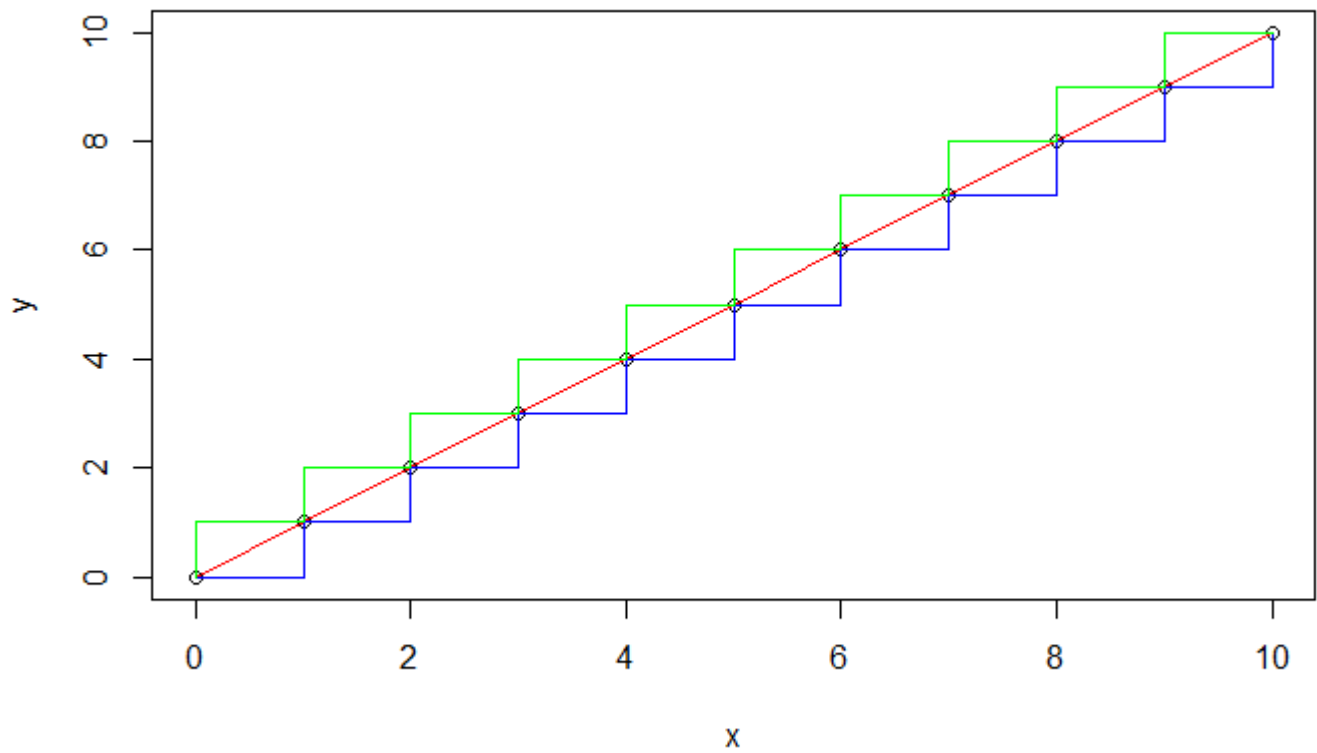
Section 5.2.7

[Hide](#)

```
x<-0:10  
y<-0:10  
plot(x,y)  
lines(x,y,col="red")
```

[Hide](#)

```
lines(x,y,col="blue",type="s")  
lines(x,y,col="green",type="S")
```



Section 5.3

[Hide](#)

```
plot(0:10,0:10,xlab="",ylab="",xaxt="n",yaxt="n",type="n")
rect(6,6,9,9)
```



Section 5.3.1

[Hide](#)

```
plot(0:10,0:10,xlab="",ylab="",xaxt="n",yaxt="n",type="n")
rect(6,6,9,9)
```

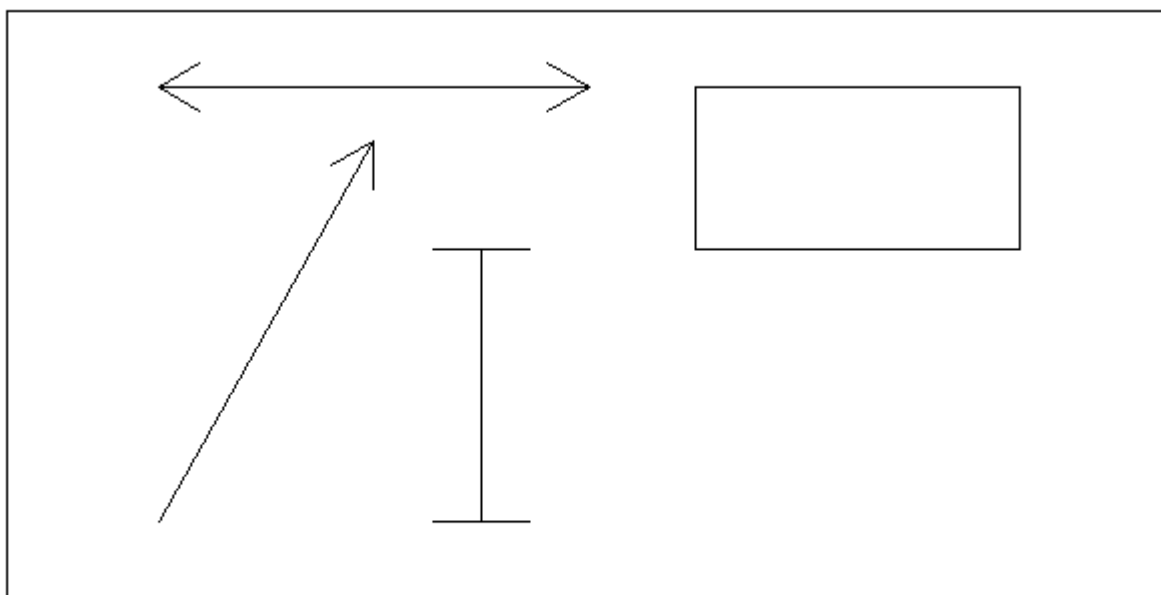
[Hide](#)

```
corners <- function(){
  coos <- c(unlist(locator(1)),unlist(locator(1)))
  rect(coos[1],coos[2],coos[3],coos[4])
}

corners()
arrows(1,1,3,8)
```

[Hide](#)

```
arrows(1,9,5,9,code=3)
arrows(4,1,4,6,code=3,angle=90)
```



[Hide](#)

```
click.arrows <- function(){
  coos <- c(unlist(locator(1)),unlist(locator(1)))
  arrows(coos[1],coos[2],coos[3],coos[4])
}

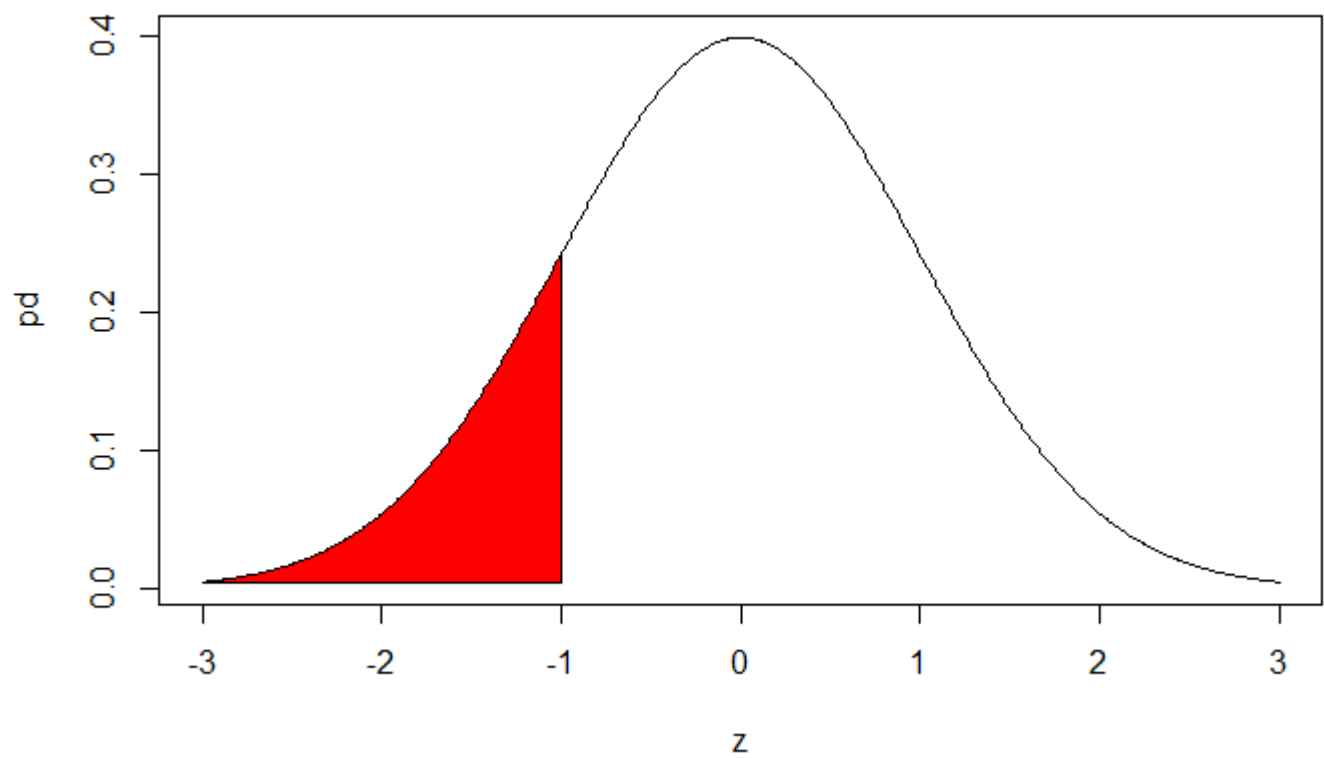
click.arrows()
```

```
Error in arrows(coos[1], coos[2], coos[3], coos[4]) :
  invalid first argument
```

Section 5.3.2

[Hide](#)

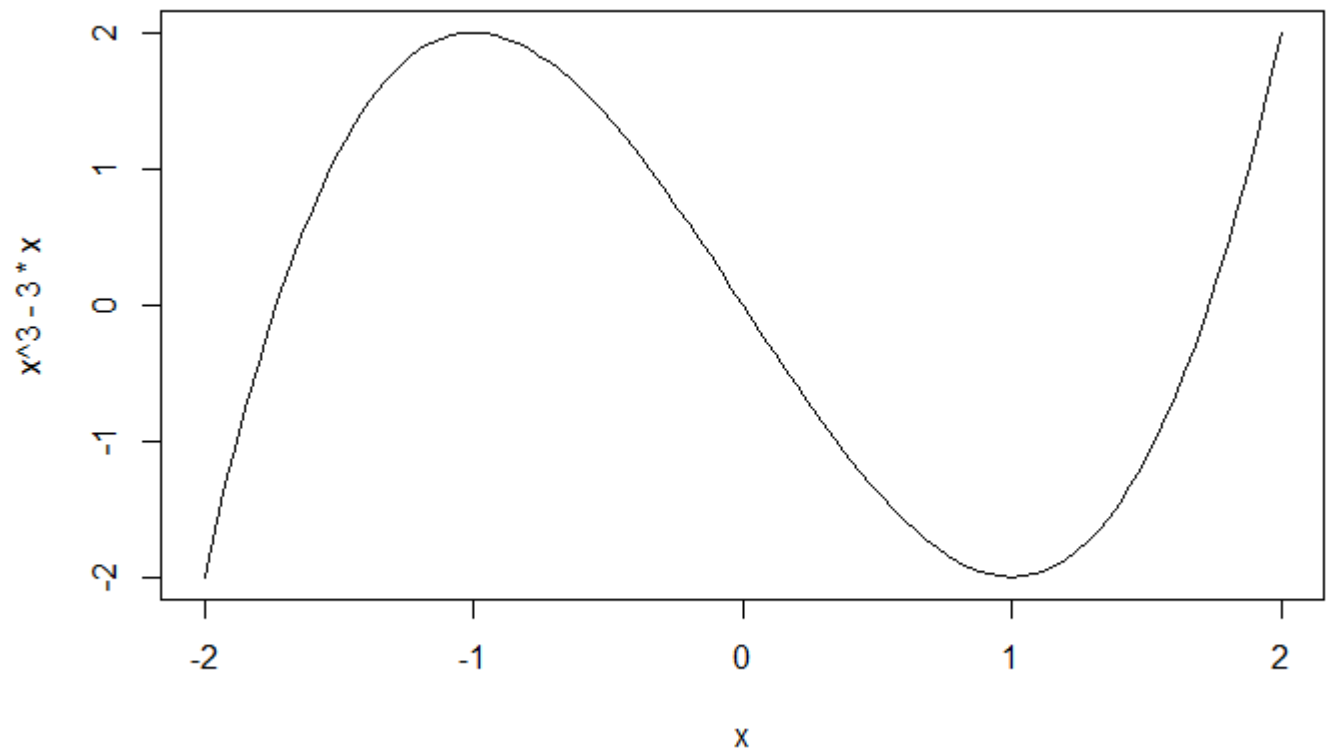
```
z <- seq(-3,3,0.01)
pd <- dnorm(z)
plot(z,pd,type="l")
polygon(c(z[z<=-1],-1),c(pd[z<=-1],pd[z==3]),col="red")
```



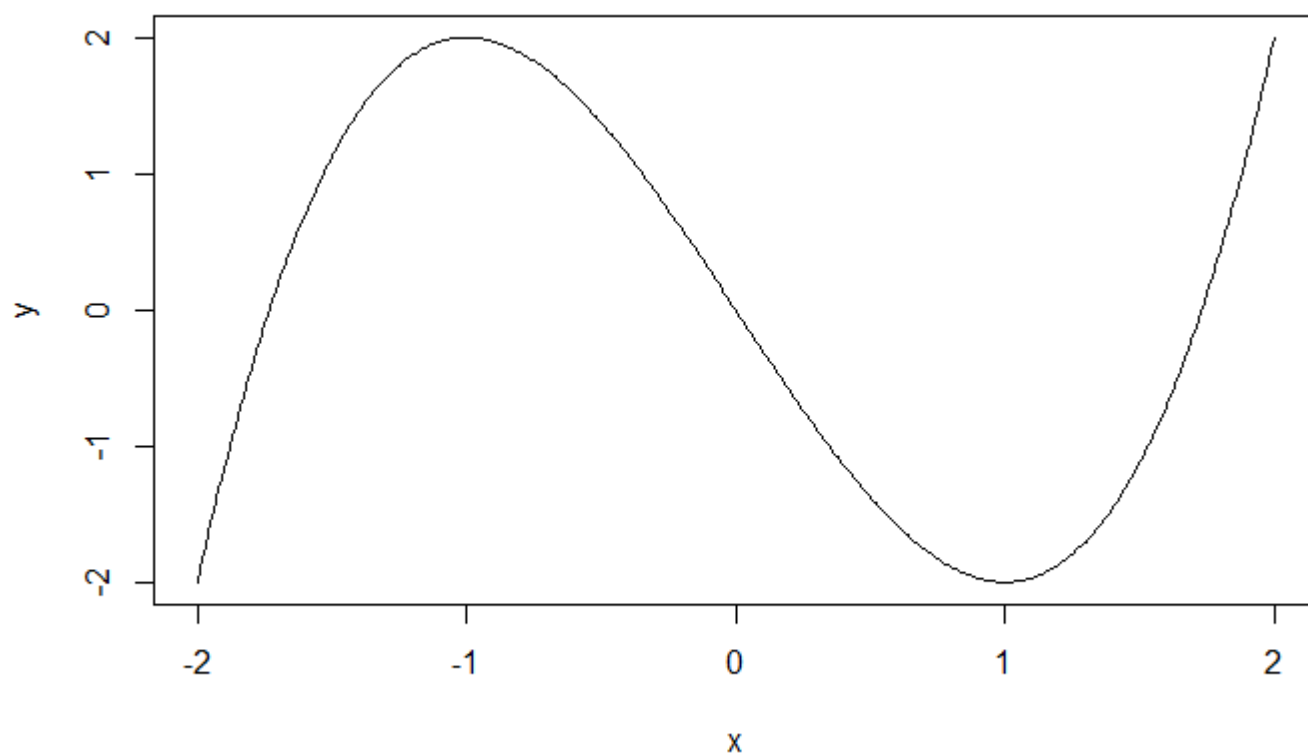
Section 5.4

[Hide](#)

```
curve(x^3-3*x, -2, 2)
```

[Hide](#)

```
x <- seq(-2,2,0.01)
y <- x^3-3*x
plot(x,y,type="l")
```



Section 5.4.1

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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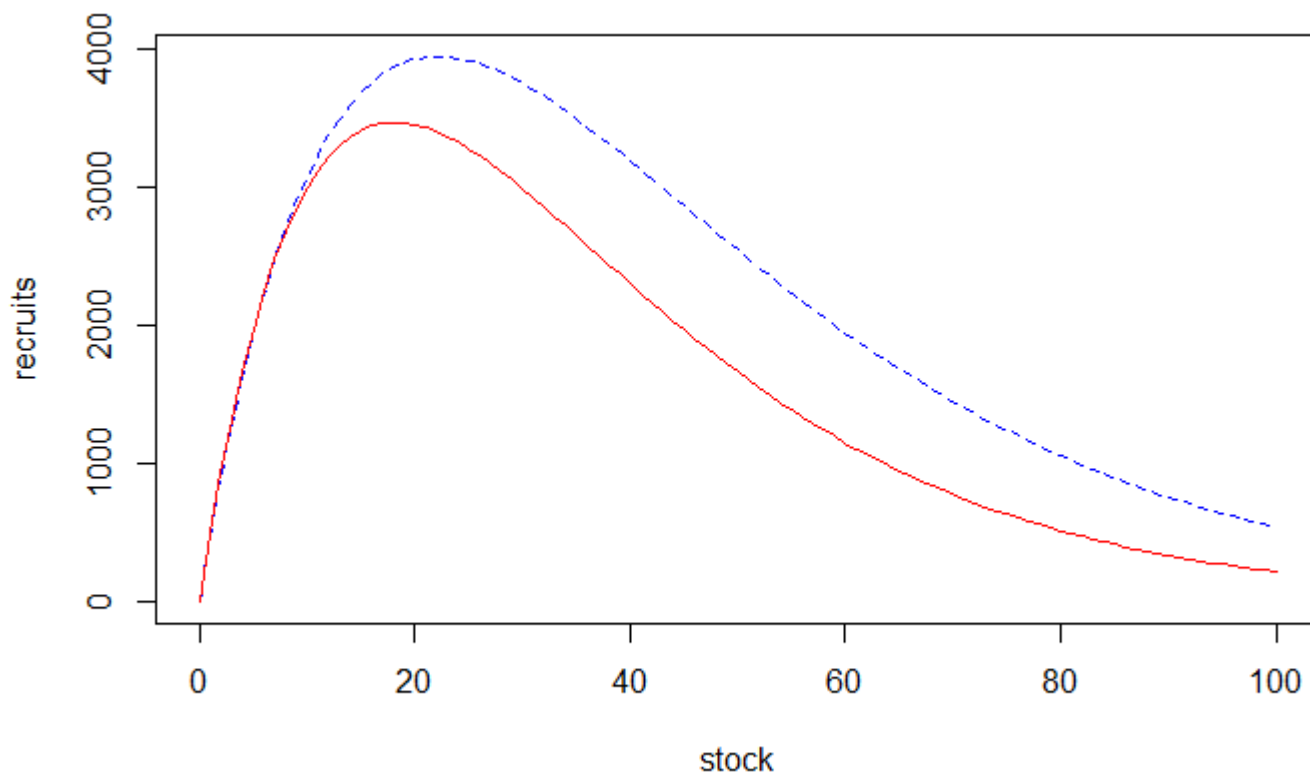
[Hide](#)

```
xv <- 0:100
yA <- 482*xv*exp(-0.045*xv)
yB <- 518*xv*exp(-0.055*xv)

plot(c(xv,xv),c(yA,yB),xlab="stock",ylab="recruits",type="n")
lines(xv,yA,lty=2,col="blue")
```

[Hide](#)

```
lines(xv,yB,lty=1,col="red")
```



Hide

```
# setwd("F:/JunYe_Files/Jun_2016Spring_Course/Spring2016_Advanced_Computinbg/therbook")
#info <- read.table("plotfit.txt",header=T)
#info <- read.table("c:\\temp\\plotfit.txt",header=T)

# I created a new data plotfit_new where I use xxx and yyy as names
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
info <- read.table("plotfit_new.txt",header=F)
```

cannot open file 'plotfit_new.txt': No such file or directoryError in file(file, "rt") : cannot open the connection

Section 5.4.3

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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Hide

```
data <- read.table("jaws.txt",header=T)
attach(data)
names(data)
```

```
[1] "age"  "bone"
```

[Hide](#)

```
par(mfrow=c(2,2))

plot(age,bone,pch=16,main="lowess")
lines(lowess(age,bone),col="red")
```

[Hide](#)

```
plot(age,bone,pch=16,main="loess")
model <- loess(bone~age)
xv <- 0:50
yv <- predict(model,data.frame(age=xv))
lines(xv,yv,col="red")
```

[Hide](#)

```
library(mgcv)
```

```
Loading required package: nlme
This is mgcv 1.8-28. For overview type 'help("mgcv-package")'.
```

[Hide](#)

```
plot(age,bone,pch=16,main="gam")
```

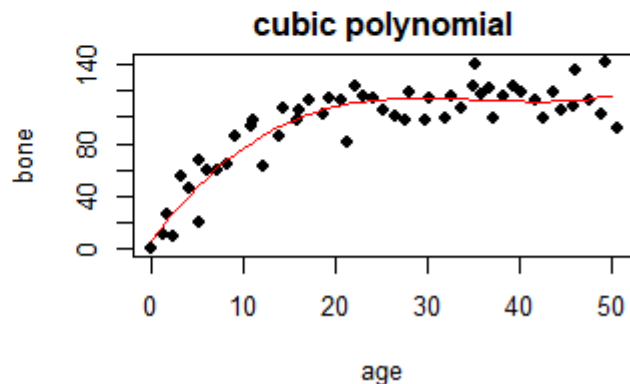
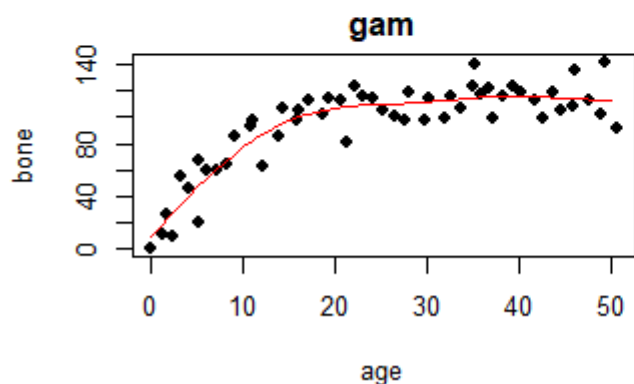
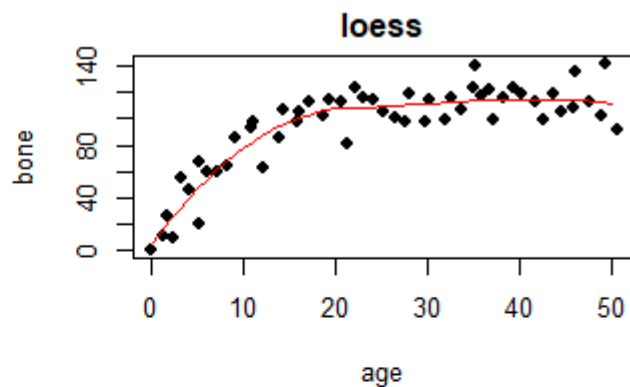
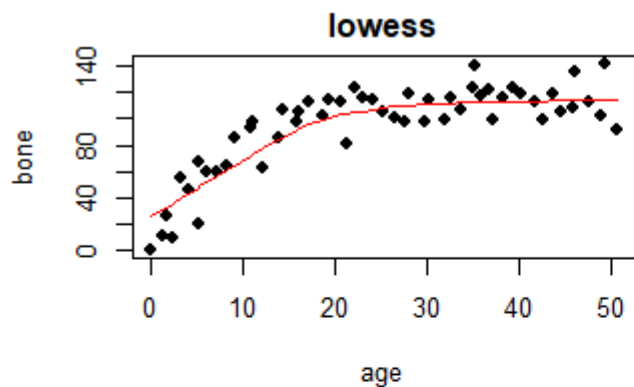
[Hide](#)

```
model <- gam(bone~s(age))
xv <- 0:50
yv <- predict(model,list(age=xv))
lines(xv,yv,col="red")

plot(age,bone,pch=16,main="cubic polynomial")
```

[Hide](#)

```
model <- lm(bone~age+I(age^2)+I(age^3))
xv <- 0:50
yv <- predict(model,list(age=xv))
lines(xv,yv,col="red")
```



Section 5.5

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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[Hide](#)

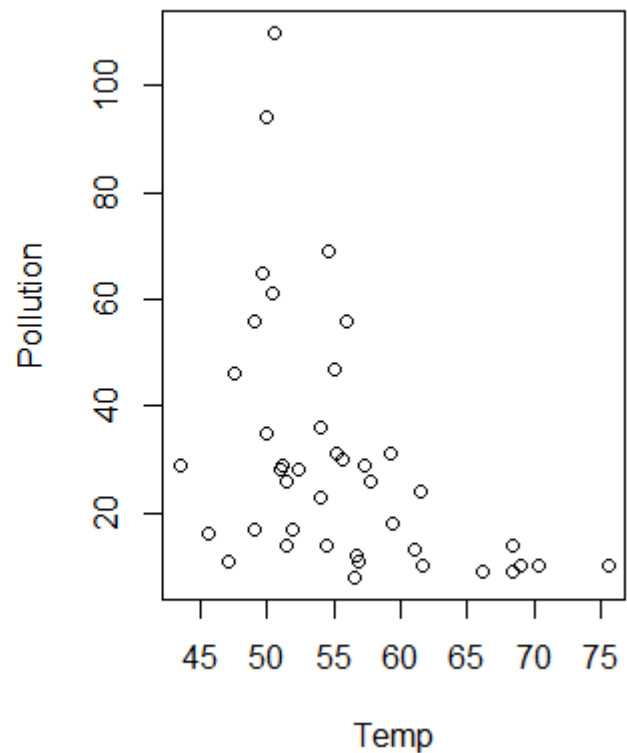
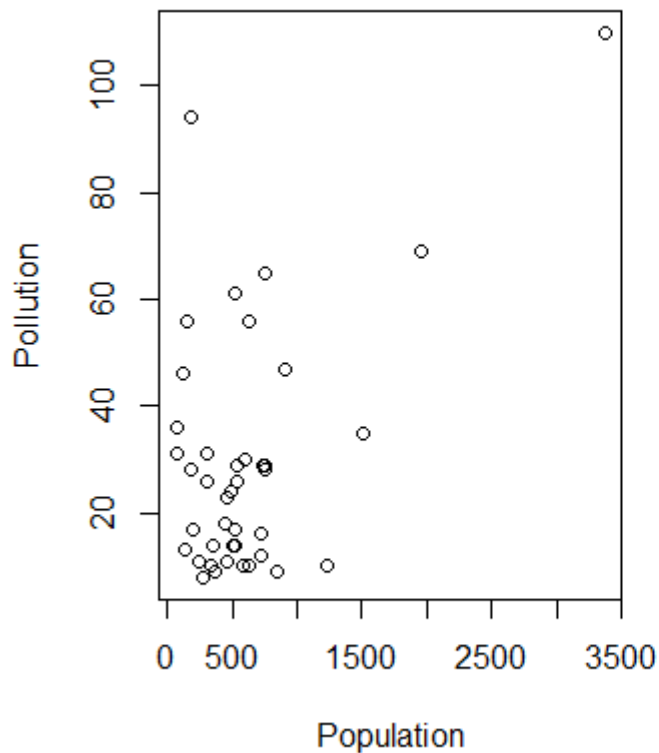
```
data <- read.table("pollute.txt",header=T)
attach(data)
```

The following objects are masked from data (pos = 3):

Industry, Pollution, Population, Rain, Temp, Wet.days, Wind

[Hide](#)

```
par(mfrow=c(1,2))
plot(Population,Pollution)
```


[Hide](#)

```
plot(Temp,Pollution)
```

```
windows(7,4)
```

[Hide](#)

```
par(mfrow=c(1,2))
plot(Population,Pollution)
```

[Hide](#)

```
plot(Temp,Pollution)
```

Section 5.6

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
weather <- read.table("SilwoodWeather.txt",header=T)
attach(weather)
```

The following object is masked `_by_ .GlobalEnv`:

month

The following objects are masked from `weather` (pos = 4):

lower, month, rain, upper, yr

Hide

```
names(weather)
```

```
[1] "upper" "lower" "rain"  "month" "yr"
```

Hide

```
month <- factor(month)
plot(month,upper)
plot(month,upper,ylab="daily maximum temperature",xlab="month")
```

Hide

```
# 5.6.1 Boxplots with notches to indicate significant differences
# 5.6.2 Barplots with error bars
trial <- read.table("compexpt.txt",header=T)
attach(trial)
```

The following objects are masked from `trial` (pos = 4):

biomass, clipping

Hide

```
names(trial)
```

```
[1] "biomass" "clipping"
```

Hide

```
means <- tapply(biomass,clipping,mean)
barplot(means,xlab="treatment",ylab="mean yield",col="green")

seBars <- function(x,y){
  model <- lm(y~factor(x))
  reps <- length(y)/length(levels(x))
  sem <- summary(model)$sigma/sqrt(reps)
  m <- as.vector(tapply(y,x,mean))
  upper <- max(m)+sem
  nn <- as.character(levels(x))
  xs <- barplot(m,ylim=c(0,upper),names=nn,
                ylab=deparse(substitute(y)),xlab=deparse(substitute(x)))
  for (i in 1:length(xs)) {
    arrows(xs[i],m[i]+sem,xs[i],m[i]-sem,angle=90,code=3,length=0.1) }
}

seBars(clipping,biomass)
```

Hide

```
windows(7,4)
par(mfrow=c(1,2))
```

Hide

```
plot(clipping,biomass)
plot(clipping,biomass,notch=T)
```

5.6.1 Boxplots with notches to indicate significant differences

5.6.2 Barplots with error bars

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
trial <- read.table("compexpt.txt",header=T)
attach(trial)
```

The following objects are masked from trial (pos = 3):

biomass, clipping

The following objects are masked from trial (pos = 5):

biomass, clipping

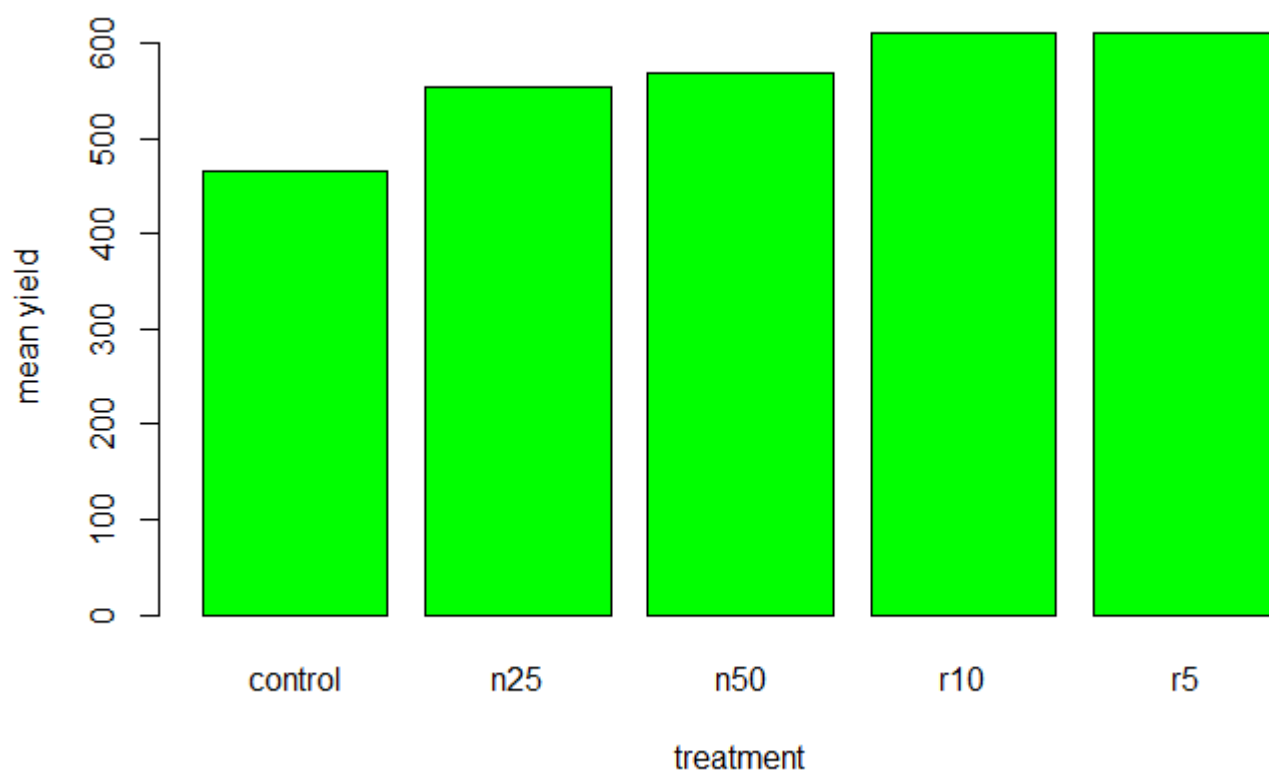
[Hide](#)

```
names(trial)
```

```
[1] "biomass" "clipping"
```

[Hide](#)

```
means <- tapply(biomass,clipping,mean)
barplot(means,xlab="treatment",ylab="mean yield",col="green")
```

[Hide](#)

```
seBars <- function(x,y){
  model <- lm(y~factor(x))
  reps <- length(y)/length(levels(x))
  sem <- summary(model)$sigma/sqrt(reps)
  m <- as.vector(tapply(y,x,mean))
  upper <- max(m)+sem
  nn <- as.character(levels(x))
  xs <- barplot(m,ylim=c(0,upper),names=nn,
               ylab=deparse(substitute(y)),xlab=deparse(substitute(x)))
  for (i in 1:length(xs)) {
    arrows(xs[i],m[i]+sem,xs[i],m[i]-sem,angle=90,code=3,length=0.1) }
}

seBars(clipping,biomass)
windows(7,4)
```

Hide

```
par(mfrow=c(1,2))
plot(clipping,biomass)
```

Hide

```
plot(clipping,biomass,notch=T)
```

Section 5.6.3

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
data <- read.table("box.txt",header=T)
attach(data)
```

The following objects are masked from data (pos = 3):

fact, response

The following object is masked from nums:

response

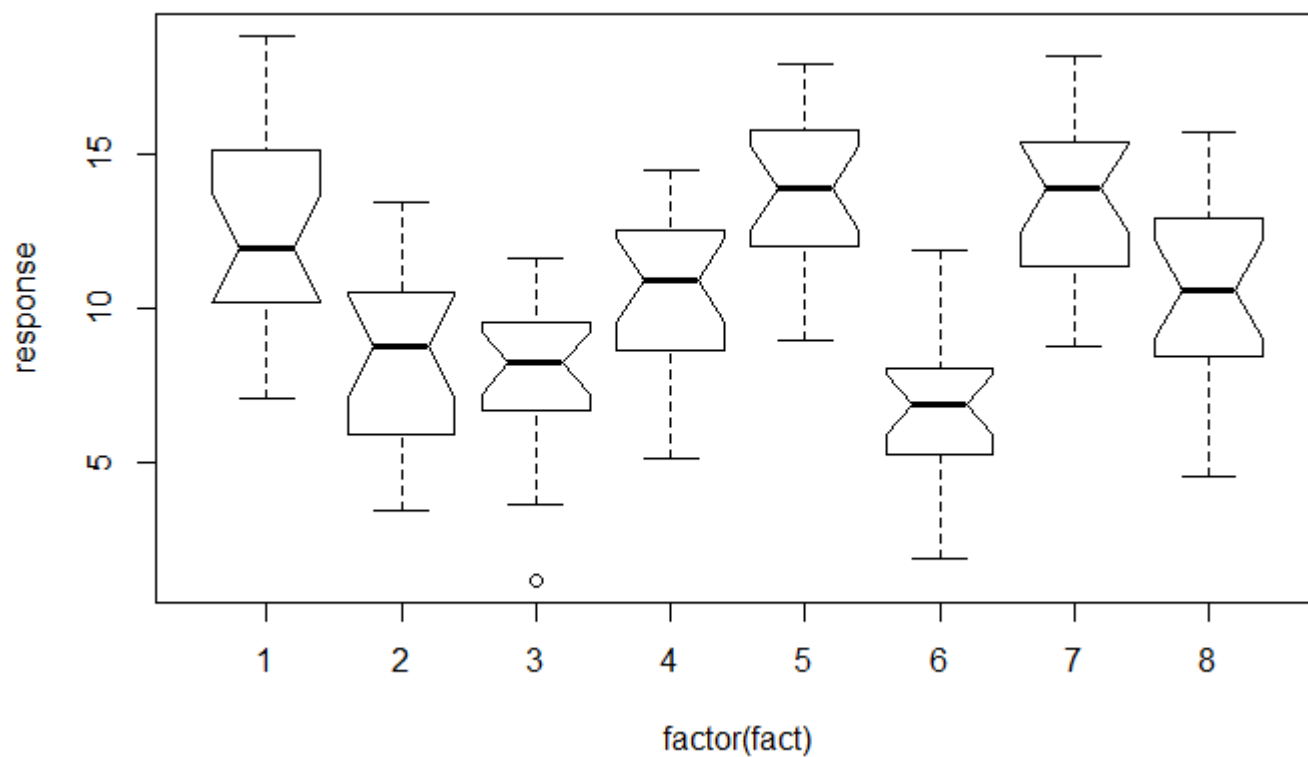
[Hide](#)

```
names(data)
```

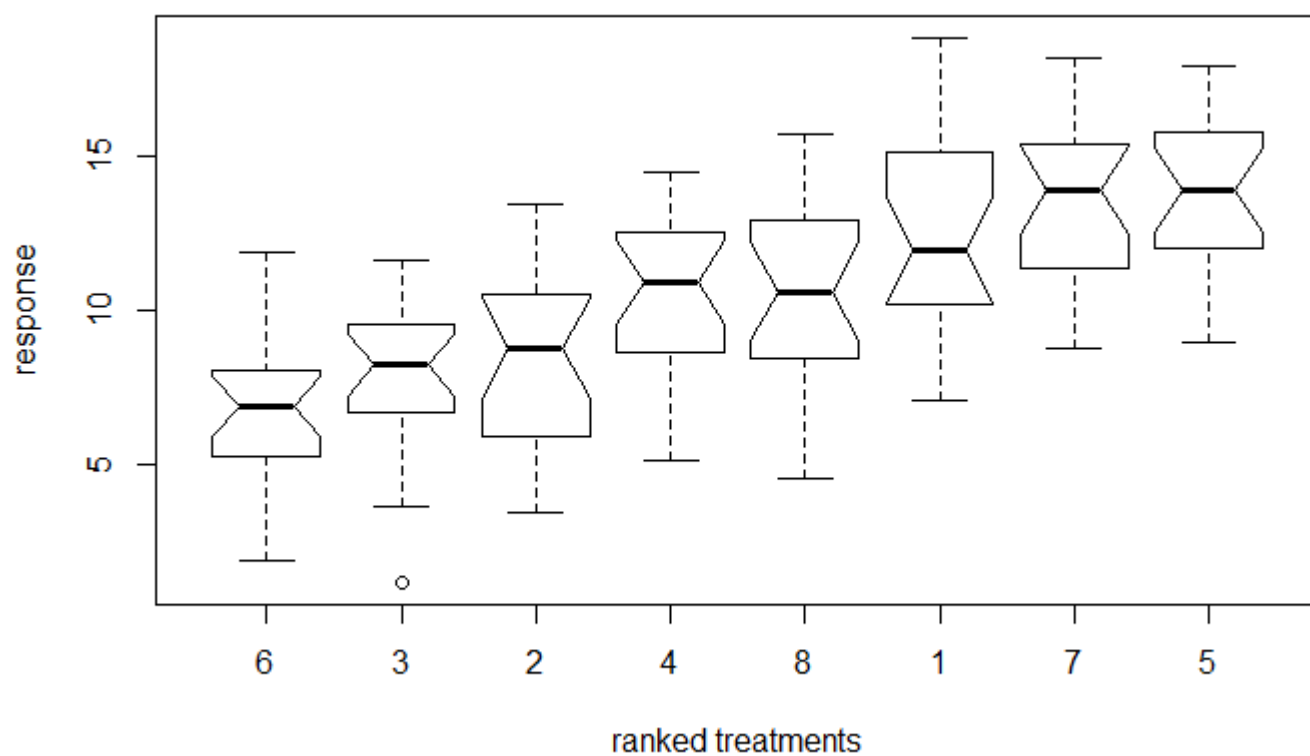
```
[1] "fact"    "response"
```

[Hide](#)

```
plot(response~factor(fact),notch=TRUE)
```

[Hide](#)

```
index <- order(tapply(response,fact,mean))
ordered <- factor(rep(index,rep(20,8)))
boxplot(response~ordered,notch=T,names=as.character(index),
        xlab="ranked treatments",ylab="response")
```

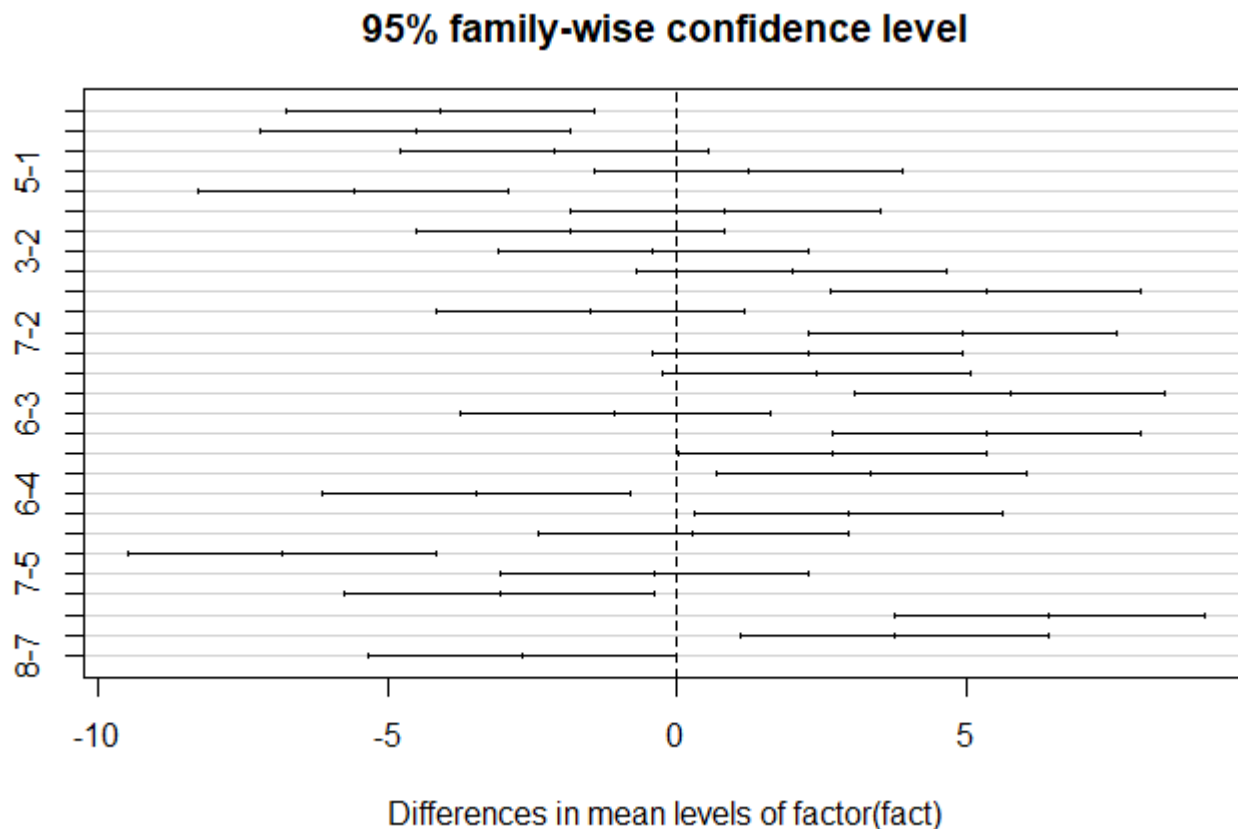

[Hide](#)

```
model <- aov(response~factor(fact))
summary(model)
```

```
          Df Sum Sq Mean Sq F value Pr(>F)
factor(fact)  7  925.7   132.24   17.48 <2e-16 ***
Residuals   152 1150.1     7.57
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

[Hide](#)

```
plot(TukeyHSD(model))
```



Section 5.6.4

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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[Hide](#)

```
data <- read.table("silwoodweather.txt",header=T)
attach(data)
```

The following object is masked `_by_` .GlobalEnv:

month

The following objects are masked from `weather` (pos = 7):

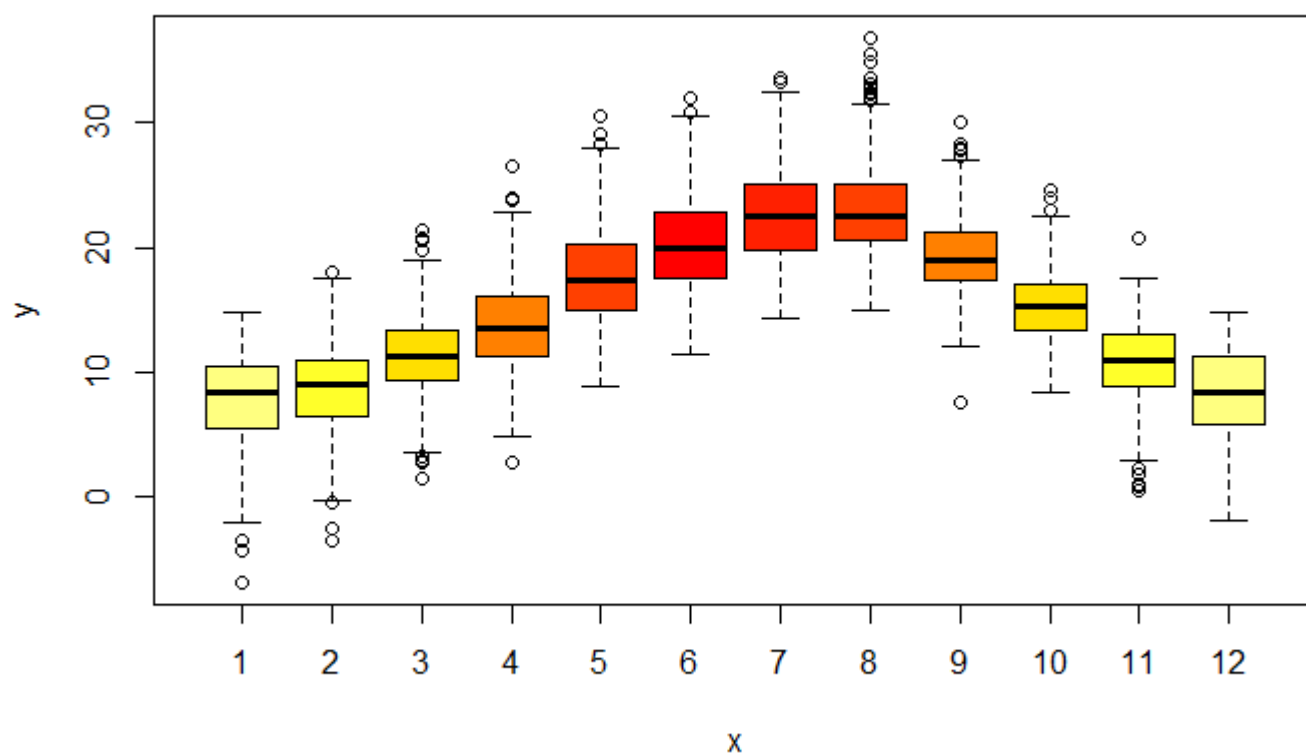
lower, month, rain, upper, yr

The following objects are masked from `weather` (pos = 9):

lower, month, rain, upper, yr

Hide

```
month <- factor(month)
season <- heat.colors(12)
temp <- c(11,10,8,5,3,1,2,3,5,8,10,11)
plot(month,upper,col=season[temp])
```



The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/ther book inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

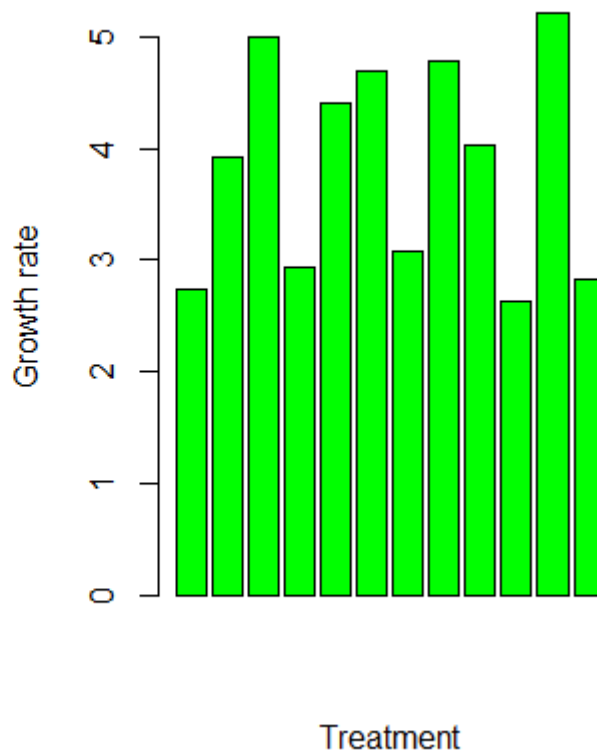
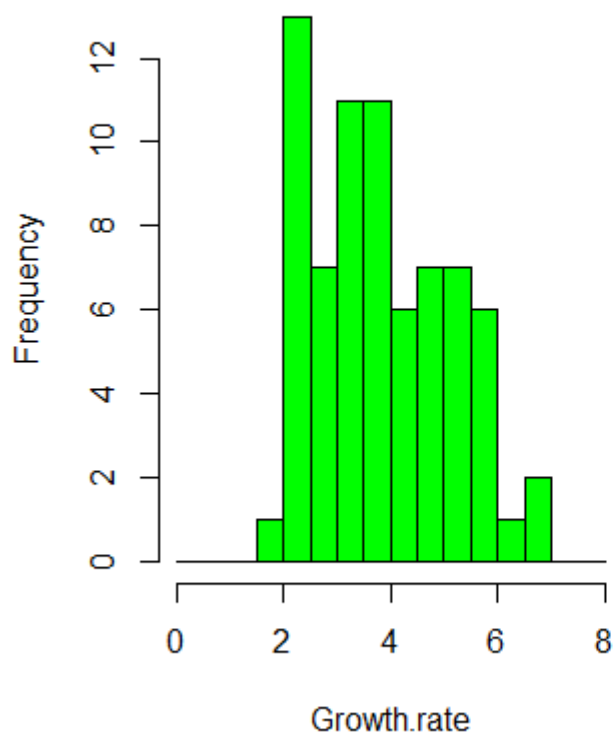
Hide

```
data<-read.table("daphnia.txt",header=T)
attach(data)
names(data)
```

```
[1] "Growth.rate" "Water"          "Detergent"    "Daphnia"
```

Hide

```
par(mfrow=c(1,2))
hist(Growth.rate,seq(0,8,0.5),col="green",main="")
y <- as.vector(tapply(Growth.rate,list(Daphnia,Detergent),mean))
barplot(y,col="green",ylab="Growth rate",xlab="Treatment")
```



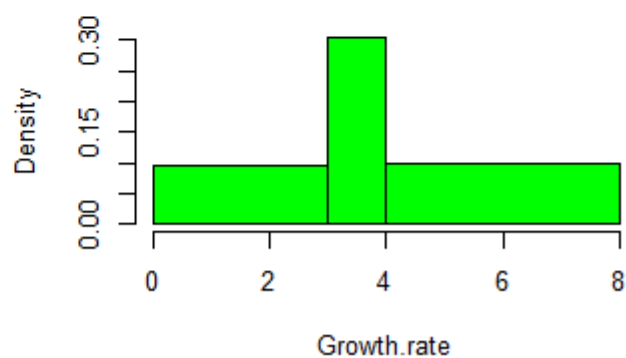
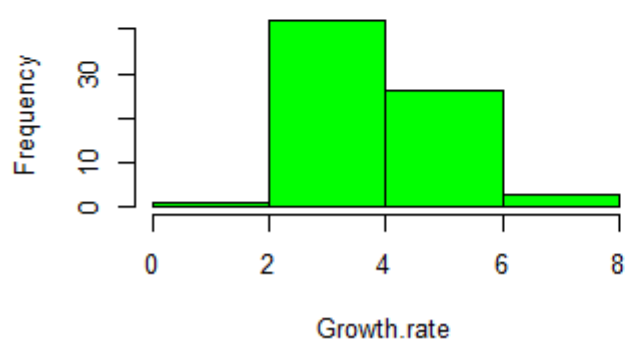
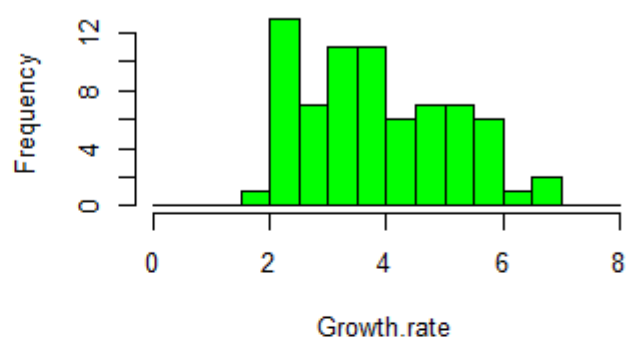
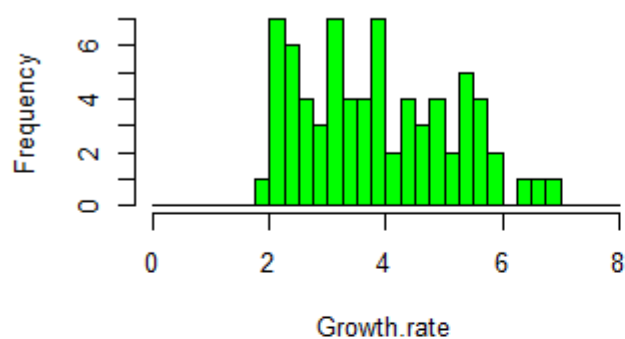
Section 5.7.2

Hide

```
par(mfrow=c(2,2))
hist(Growth.rate,seq(0,8,0.25),col="green",main="")
hist(Growth.rate,seq(0,8,0.5),col="green",main="")
```

Hide

```
hist(Growth.rate,seq(0,8,2),col="green",main="")
hist(Growth.rate,c(0,3,4,8),col="green",main="")
```



Hide

```
range(Growth.rate)
```

```
[1] 1.761603 6.918344
```

Hide

```
edges <- c(0,3,4,8)

bin <- cut(Growth.rate,edges)
bin
```

```
[1] (0,3] (0,3] (3,4] (0,3] (3,4] (4,8] (4,8] (3,4] (4,8] (0,3] (3,4] (0,3] (3,4] (4,8] (4,8]
(4,8] (4,8] (4,8] (0,3] (3,4] (3,4] (3,4]
[23] (3,4] (3,4] (3,4] (4,8] (4,8] (0,3] (0,3] (3,4] (3,4] (4,8] (4,8] (0,3] (3,4] (4,8] (0,3]
(0,3] (3,4] (3,4] (3,4] (4,8] (4,8] (4,8]
[45] (4,8] (3,4] (0,3] (3,4] (4,8] (4,8] (4,8] (3,4] (4,8] (4,8] (0,3] (3,4] (0,3] (4,8] (4,8]
(4,8] (0,3] (3,4] (4,8] (0,3] (0,3] (0,3]
[67] (4,8] (4,8] (4,8] (0,3] (0,3] (0,3]
Levels: (0,3] (3,4] (4,8]
```

Hide

```
is.factor(bin)
```

```
[1] TRUE
```

Hide

```
table(bin)
```

```
bin
(0,3] (3,4] (4,8]
    21    22    29
```

Hide

```
sum(table(bin))
```

```
[1] 72
```

Hide

```
diff(edges)
```

```
[1] 3 1 4
```

Hide

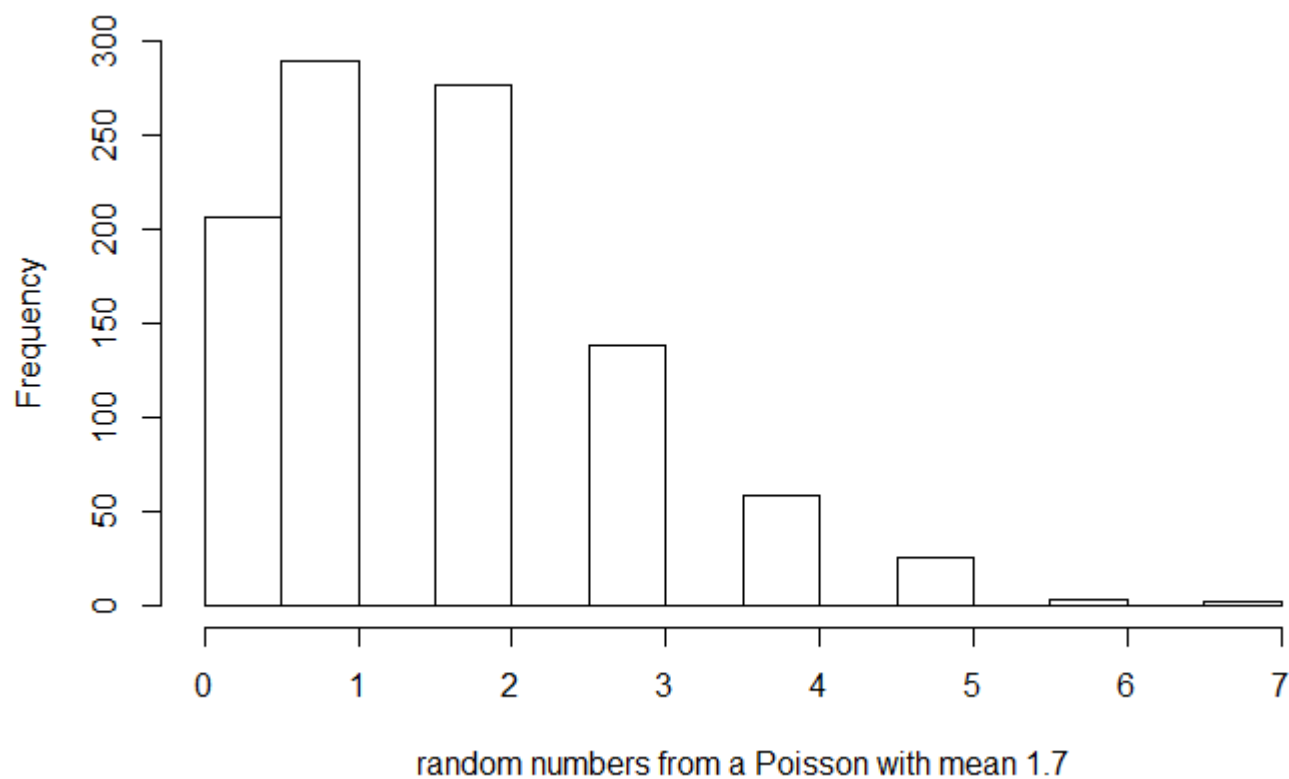
```
(table(bin)/sum(table(bin)))/diff(edges)
```

```
bin
    (0,3]    (3,4]    (4,8]
0.09722222 0.30555556 0.10069444
```

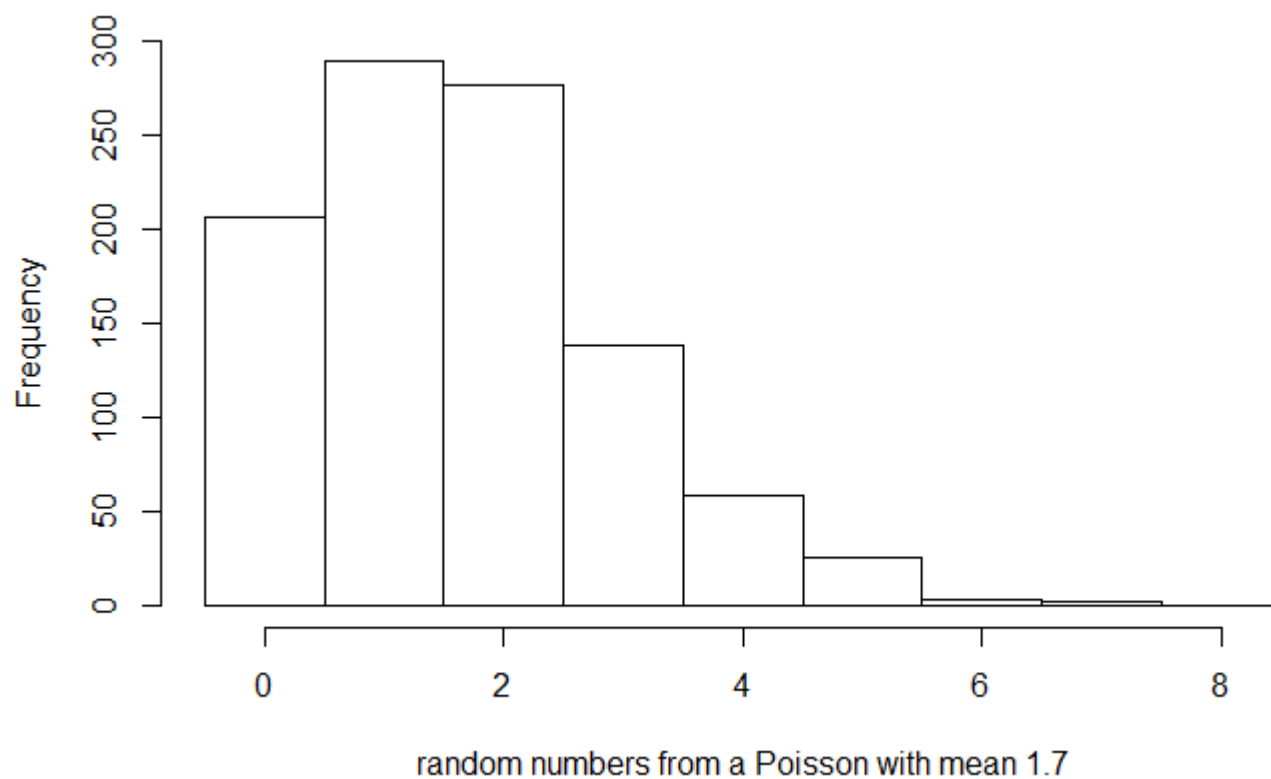
Hide

Section 5.7.3

```
values <- rpois(1000,1.70)
hist(values,main="",xlab="random numbers from a Poisson with mean 1.7")
```

[Hide](#)

```
hist(values,breaks=(-0.5:8.5),main="",
      xlab="random numbers from a Poisson with mean 1.7")
```



Section 5.7.4

[Hide](#)

```
y <- rbinom(158,mu=1.5,size=1)
bks <- -0.5:(max(y)+0.5)
hist(y,bks,main="")
mean(y)
```

```
[1] 1.310127
```

[Hide](#)

```
var(y)
```

```
[1] 3.208941
```

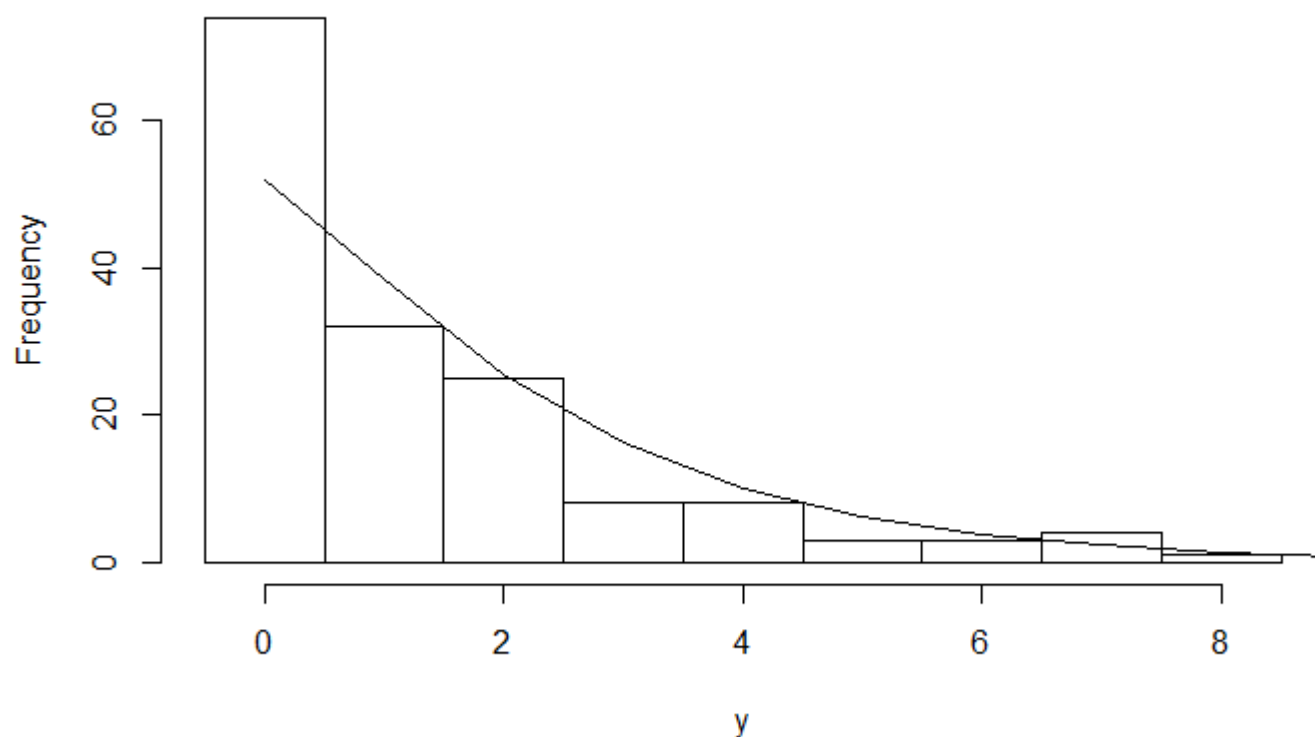
[Hide](#)

```
mean(y)^2/(var(y)-mean(y))
```

```
[1] 0.903949
```

[Hide](#)

```
xs <- 0:11
ys <- dnbinom(xs,size=1.2788,mu=1.772)
lines(xs,ys*158)
```



Section 5.7.5

[Hide](#)

```
library(MASS)
attach(faithful)

(max(eruptions)-min(eruptions))/(2*(1+log(length(eruptions),base=2)))
```

```
[1] 0.192573
```

[Hide](#)

```
windows(7,4)
par(mfrow=c(1,2))
hist(eruptions,15,freq=FALSE,main="",col=27)
lines(density(eruptions,width=0.6,n=200))
```

[Hide](#)

```
truehist(eruptions,nbins=15,col=27)
lines(density(eruptions,n=200))
```

Section 5.7.6

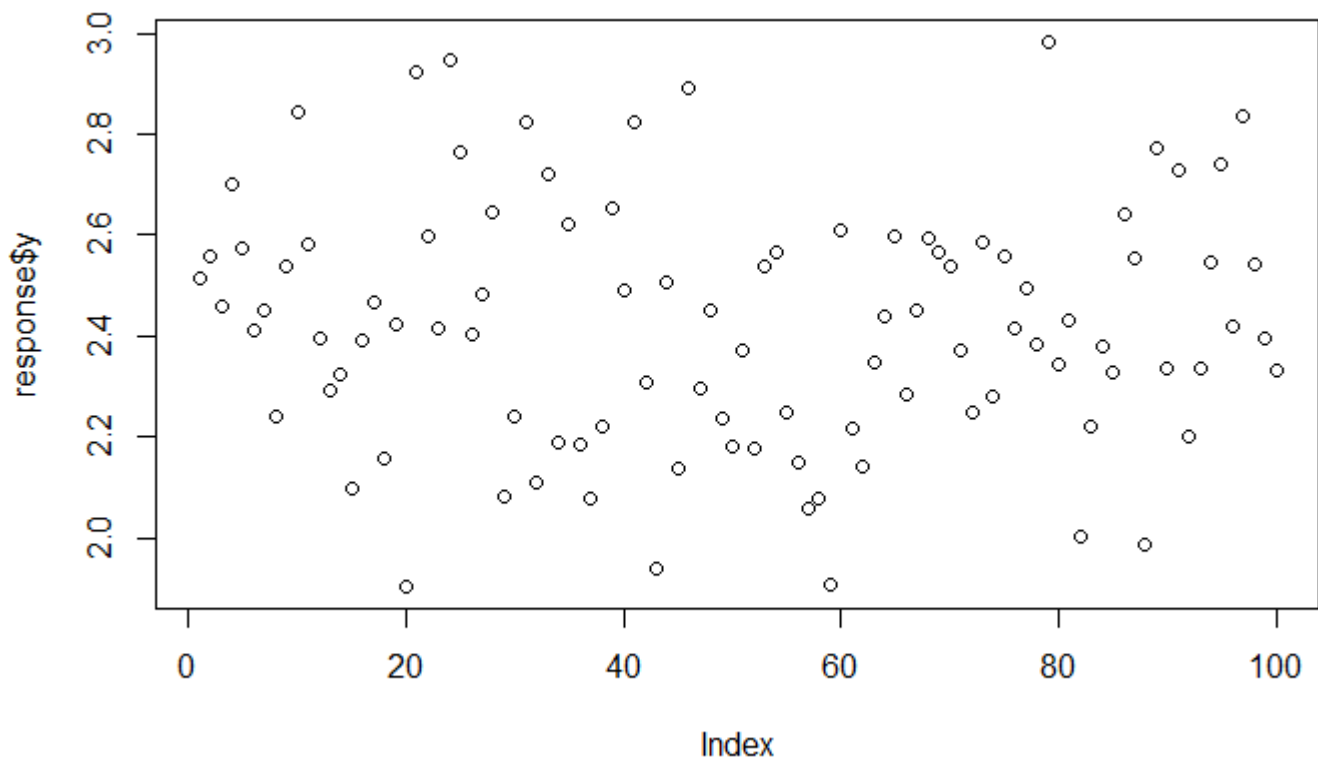
[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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[Hide](#)

```
response <- read.table("das.txt",header=T)  
plot(response$y)
```

[Hide](#)

```
which(response$y > 15)
```

```
integer(0)
```

[Hide](#)

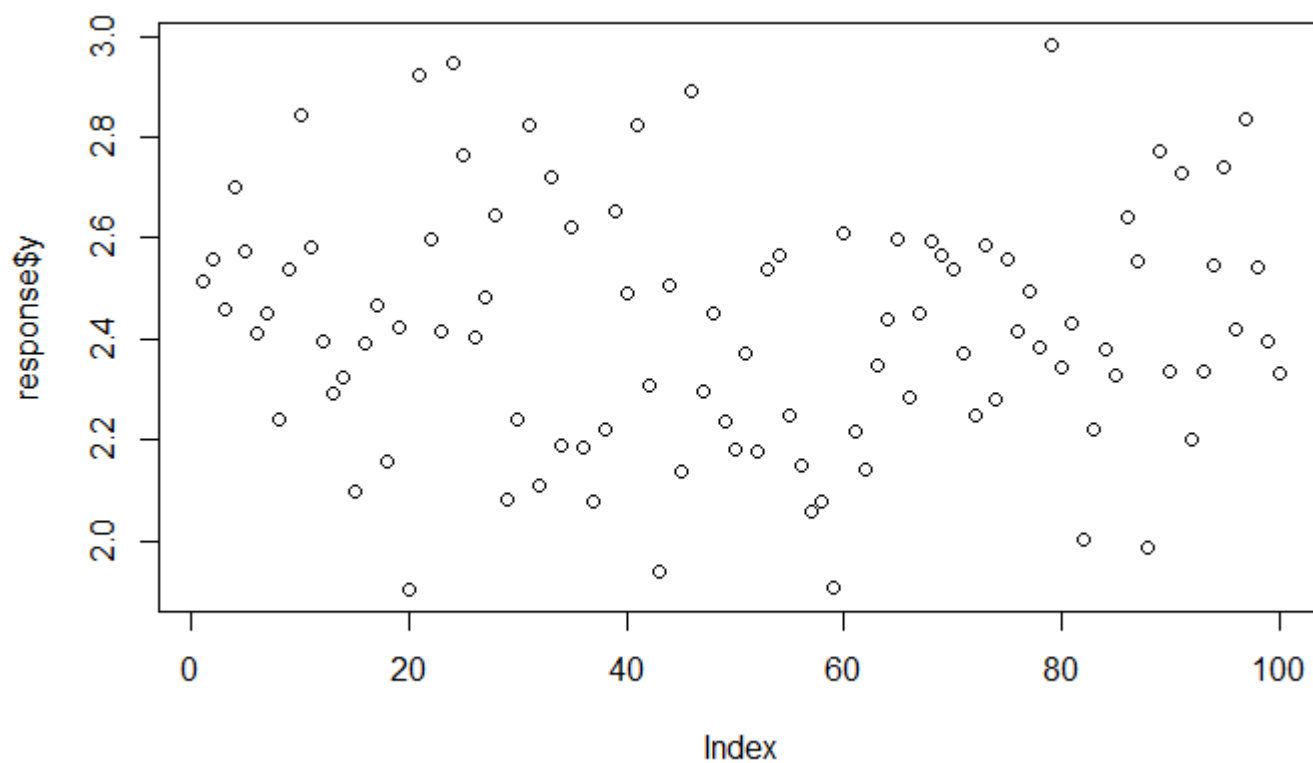
```
response$y[50]
```

```
[1] 2.179386
```

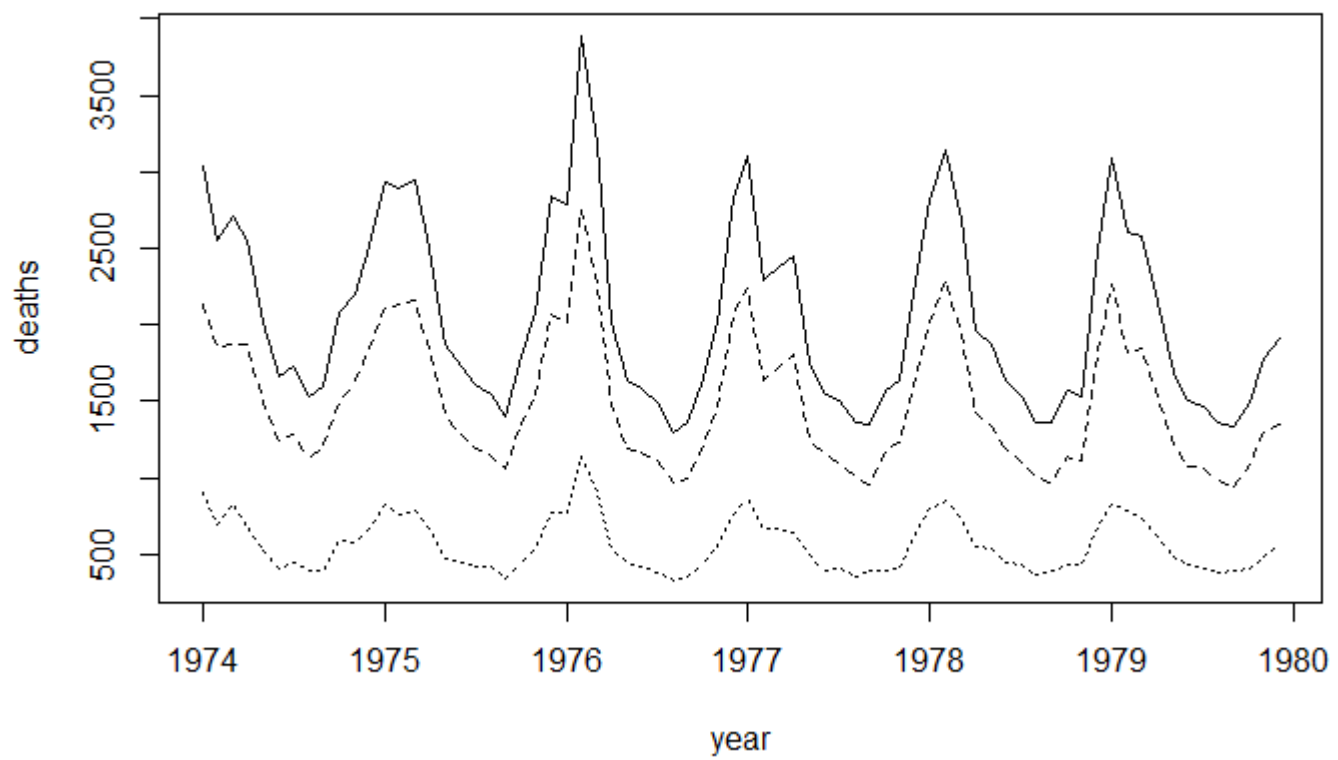
[Hide](#)

```
response$y[50] <- 2.179386
```

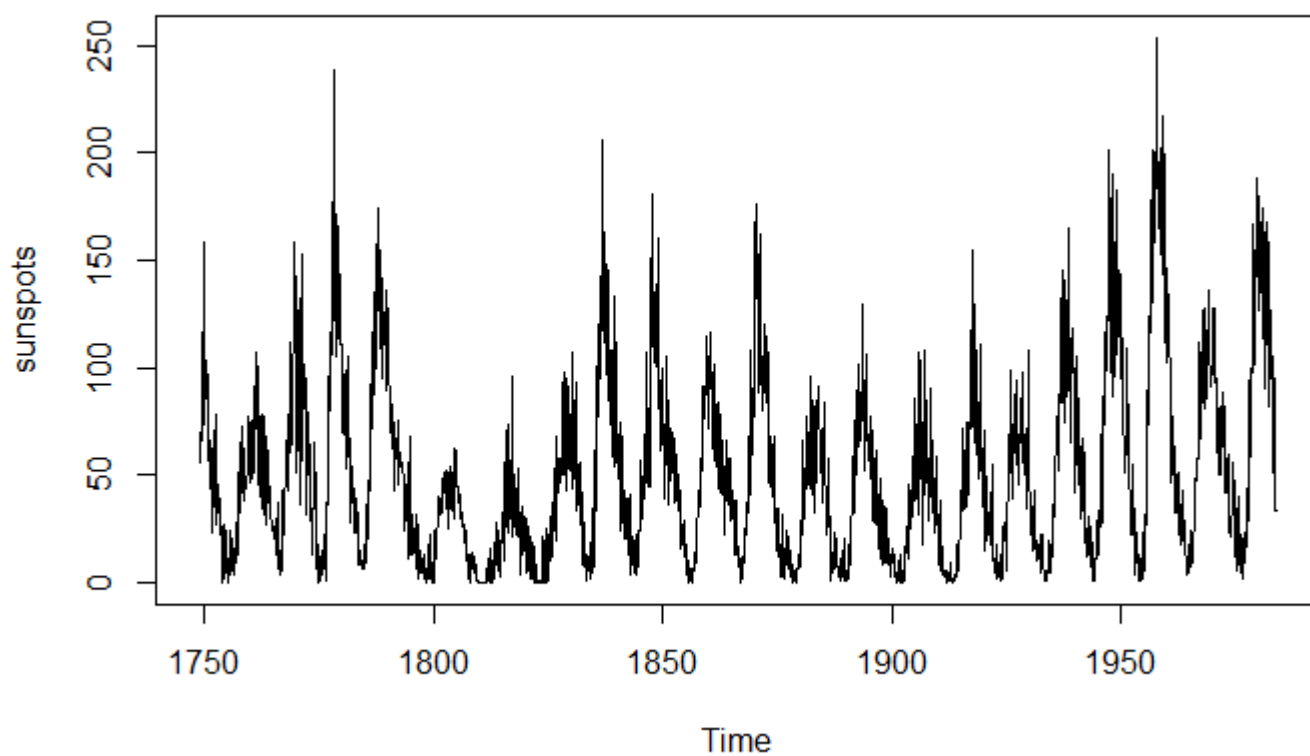
```
plot(response$y)
```

[Hide](#)

```
data(UK LungDeaths)
ts.plot(ldeaths, mdeaths, fdeaths, xlab="year", ylab="deaths", lty=c(1:3))
```


[Hide](#)

```
data(sunspots)
plot(sunspots)
```

[Hide](#)

```
class(sunspots)
```

```
[1] "ts"
```

[Hide](#)

```
is.ts(sunspots)
```

```
[1] TRUE
```

[Hide](#)

```
str(sunspots)
```

```
Time-Series [1:2820] from 1749 to 1984: 58 62.6 70 55.7 85 83.5 94.8 66.3 75.9 75.5 ...
```

Section 5.7.8

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

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Hide

```
data <- read.csv("piedata.csv")
data
```

names <fctr>	amounts <int>
coal	4
oil	2
gas	1
oil shales	3
methyl clathrates	6
5 rows	

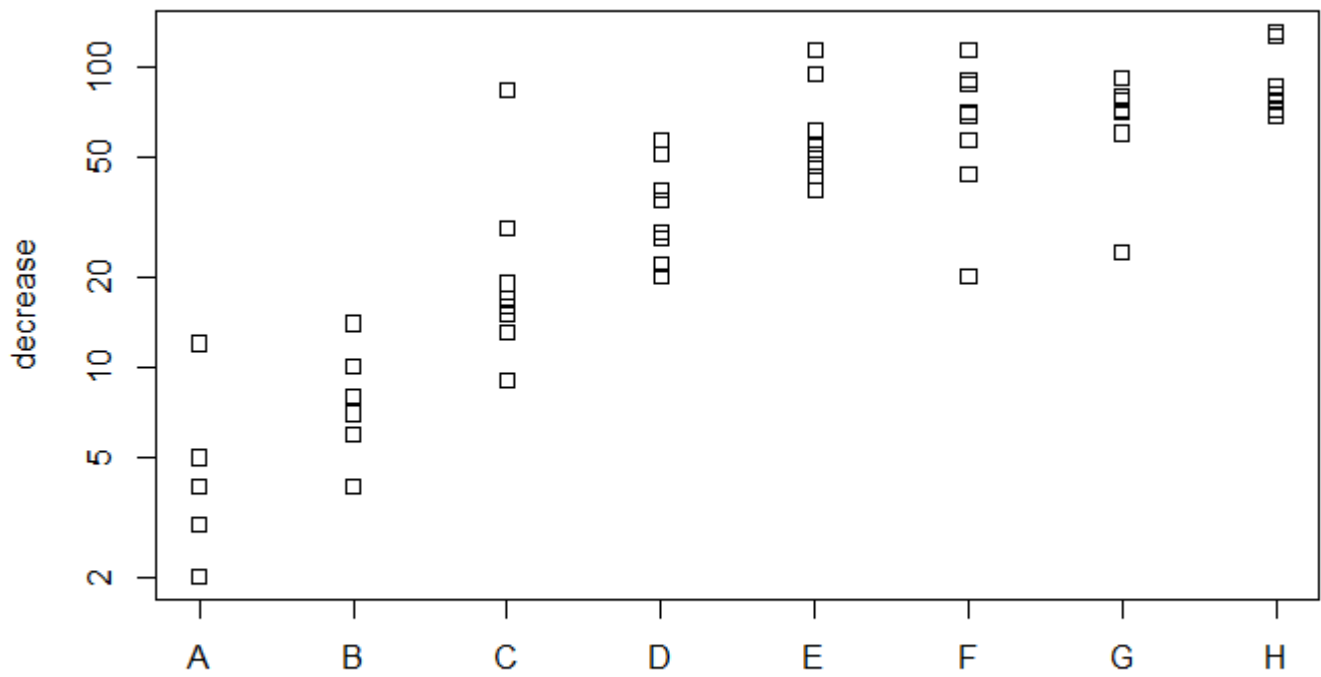
Hide

NA

Section 5.7.9

Hide

```
data(OrchardSprays)
with(OrchardSprays,
     stripchart(decrease ~ treatment,
                ylab = "decrease", vertical = TRUE, log = "y"))
```



Section 5.7.10

[Hide](#)

```

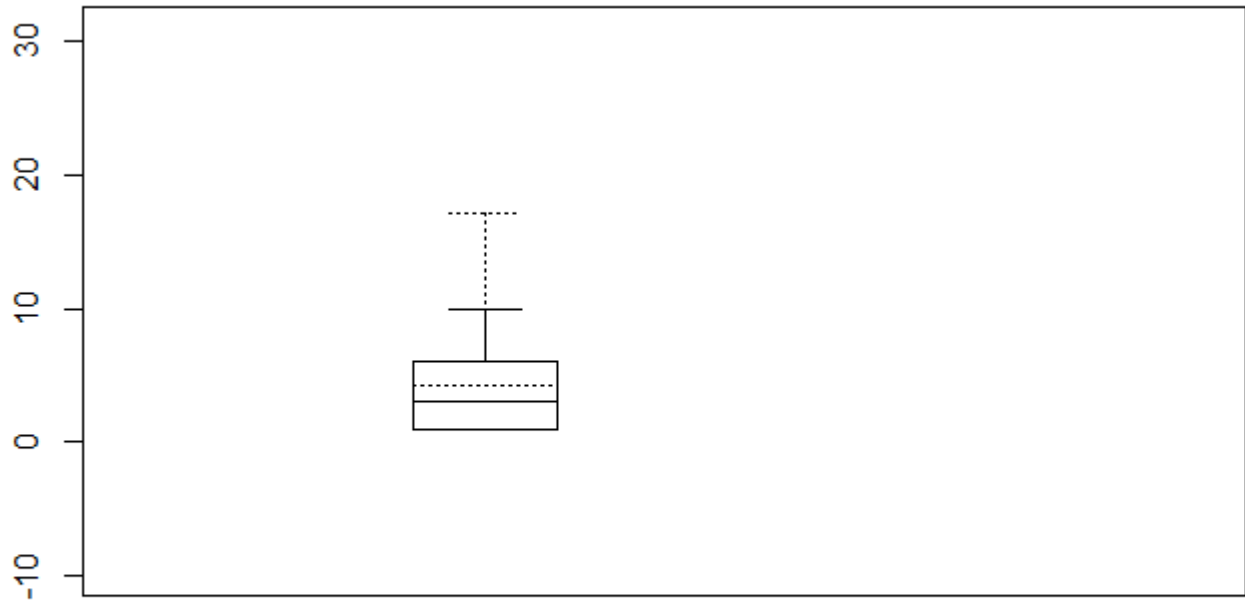
normal.plot <- function(y) {
  s <- sd(y)
  plot(c(0,3),c(min(0,mean(y)-s * 4*
                  qnorm(0.75)),max(y)),xaxt="n",xlab="",type="n",ylab="")
  # for your data's boxes and whiskers, centred at x = 1
  top <- quantile(y,0.75)
  bottom <- quantile(y,0.25)
  w1u <- quantile(y,0.91)
  w2u <- quantile(y,0.98)
  w1d <- quantile(y,0.09)
  w2d <- quantile(y,0.02)
  rect(0.8,bottom,1.2,top)
  lines(c(0.8,1.2),c(mean(y),mean(y)),lty=3)
  lines(c(0.8,1.2),c(median(y),median(y)))
  lines(c(1,1),c(top,w1u))
  lines(c(0.9,1.1),c(w1u,w1u))
  lines(c(1,1),c(w2u,w1u),lty=3)
  lines(c(0.9,1.1),c(w2u,w2u),lty=3)
  ou <- length(y[y>w2u])
  points(rep(1,nou),jitter(y[y>w2u]))
  lines(c(1,1),c(bottom,w1d))
  lines(c(0.9,1.1),c(w1d,w1d))
  lines(c(1,1),c(w2d,w1d),lty=3)
  lines(c(0.9,1.1),c(w2d,w2d),lty=3)
  nod <- length(y[y<w2d])
  points(rep(1,nod),jitter(y[y<w2d]))
  #for the normal box and whiskers, centred at x = 2
  n75 <- mean(y)+ s * qnorm(0.75)
  n25 <- mean(y)- s * qnorm(0.75)
  n91 <- mean(y)+ s * 2* qnorm(0.75)
  n98 <- mean(y)+ s * 3* qnorm(0.75)
  n9 <- mean(y)- s * 2* qnorm(0.75)
  n2 <- mean(y)- s * 3* qnorm(0.75)
  rect(1.8,n25,2.2,n75)
  lines(c(1.8,2.2),c(mean(y),mean(y)),lty=3)
  lines(c(2,2),c(n75,n91))
  lines(c(1.9,2.1),c(n91,n91))
  lines(c(2,2),c(n98,n91),lty=3)
  lines(c(1.9,2.1),c(n98,n98),lty=3)
  lines(c(2,2),c(n25,n9))
  lines(c(1.9,2.1),c(n9,n9))
  lines(c(2,2),c(n9,n2),lty=3)
  lines(c(1.9,2.1),c(n2,n2),lty=3)
  lines(c(1.2,1.8),c(top,n75),lty=3,col="gray")
  lines(c(1.1,1.9),c(w1u,n91),lty=3,col="gray")
  lines(c(1.1,1.9),c(w2u,n98),lty=3,col="gray")
  lines(c(1.2,1.8),c(bottom,n25),lty=3,col="gray")
  lines(c(1.1,1.9),c(w1d,n9),lty=3,col="gray")
  lines(c(1.1,1.9),c(w2d,n2),lty=3,col="gray")
  # label the two boxes
  axis(1,c(1,2),c("data","normal")) }

y <- rnbino(100,1,0.2)

```

```
normal.plot(y)
```

```
Error in points(rep(1, nou), jitter(y[y > w2u])) : object 'nou' not found
```



Section 5.8.1

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

[Hide](#)

```
ozonedata <- read.table("ozone.data.txt",header=T)
attach(ozonedata)
```

The following object is masked `_by_ .GlobalEnv:`

```
temp
```

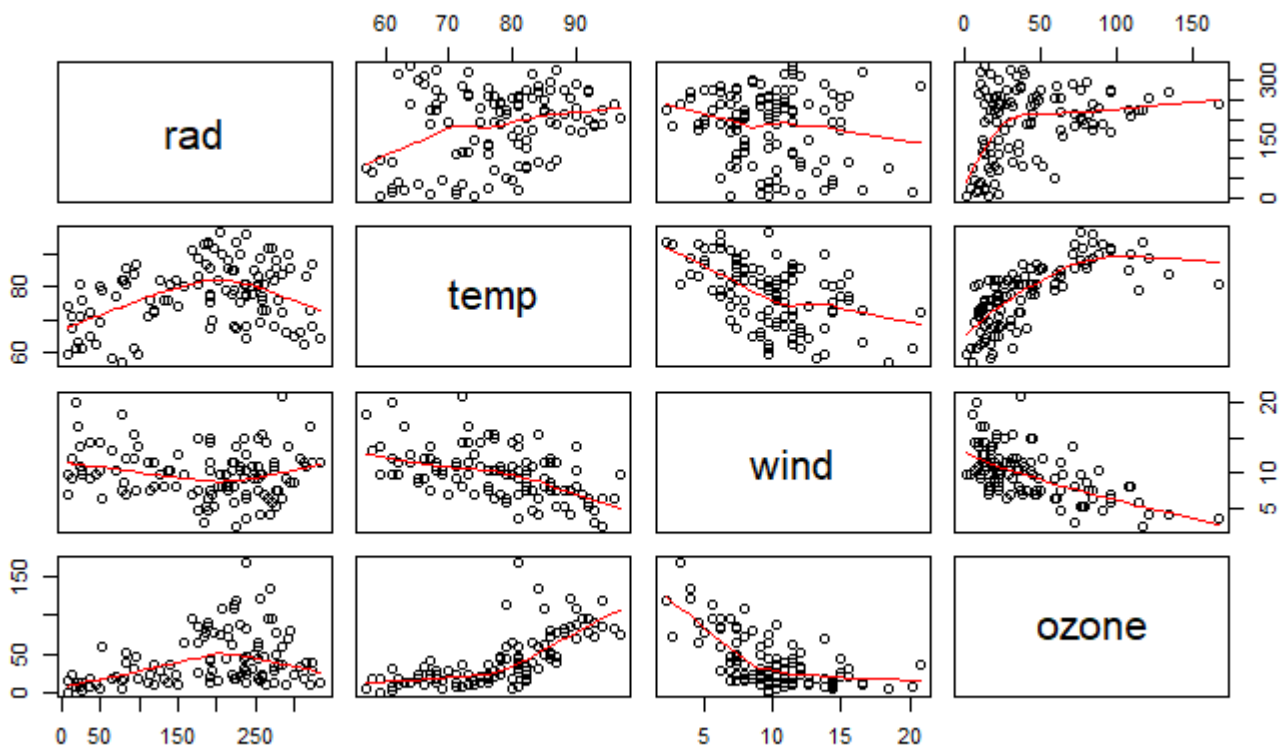
Hide

```
names(ozonedata)
```

```
[1] "rad" "temp" "wind" "ozone"
```

Hide

```
pairs(ozonedata, panel=panel.smooth)
```



Section 5.8.2

Hide

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

Hide

```
ozonedata <- read.table("ozone.data.txt", header=T)
attach(ozonedata)
```

The following object is masked `_by_` .GlobalEnv:

temp

The following objects are masked from `ozondata` (`pos = 3`):

ozone, rad, temp, wind

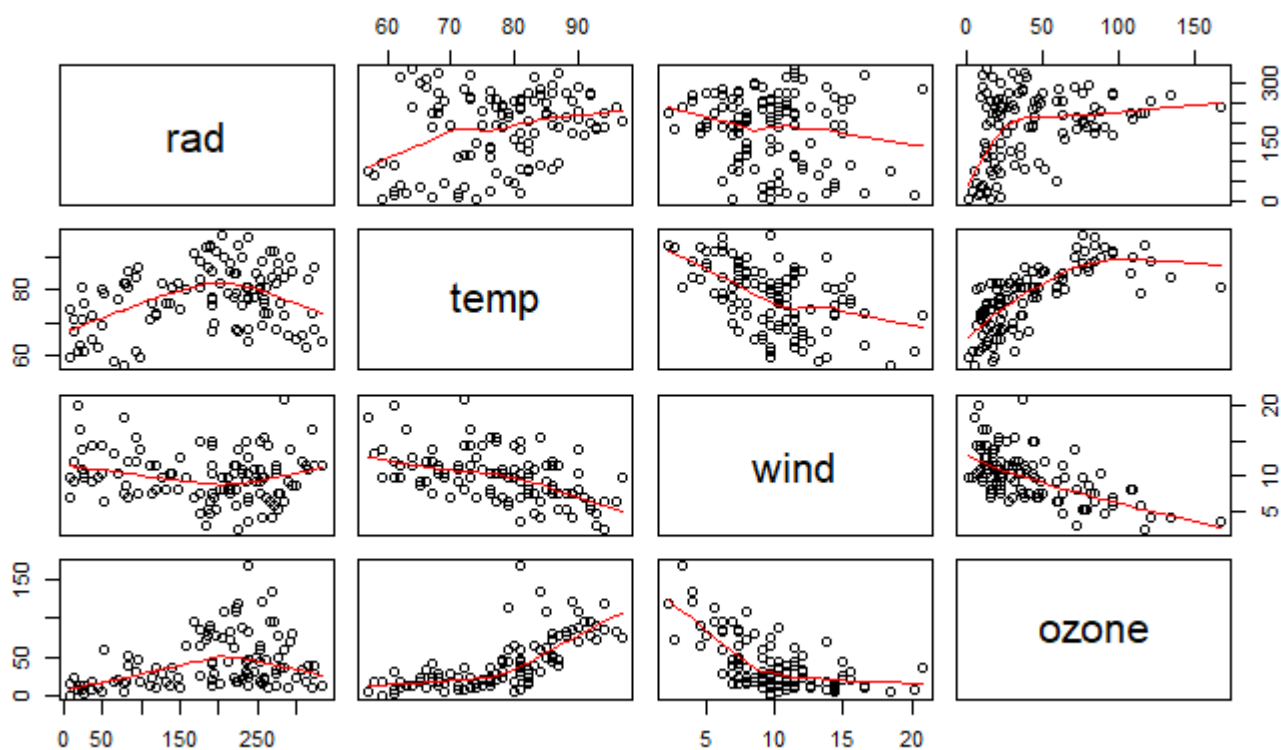
Hide

```
names(ozondata)
```

```
[1] "rad"  "temp" "wind" "ozone"
```

Hide

```
pairs(ozondata, panel=panel.smooth)
```



Hide

```
coplot(ozone~wind|temp, panel = panel.smooth)
```

Error in `bad.lengths()` : incompatible variable lengths

Section 5.8.3

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

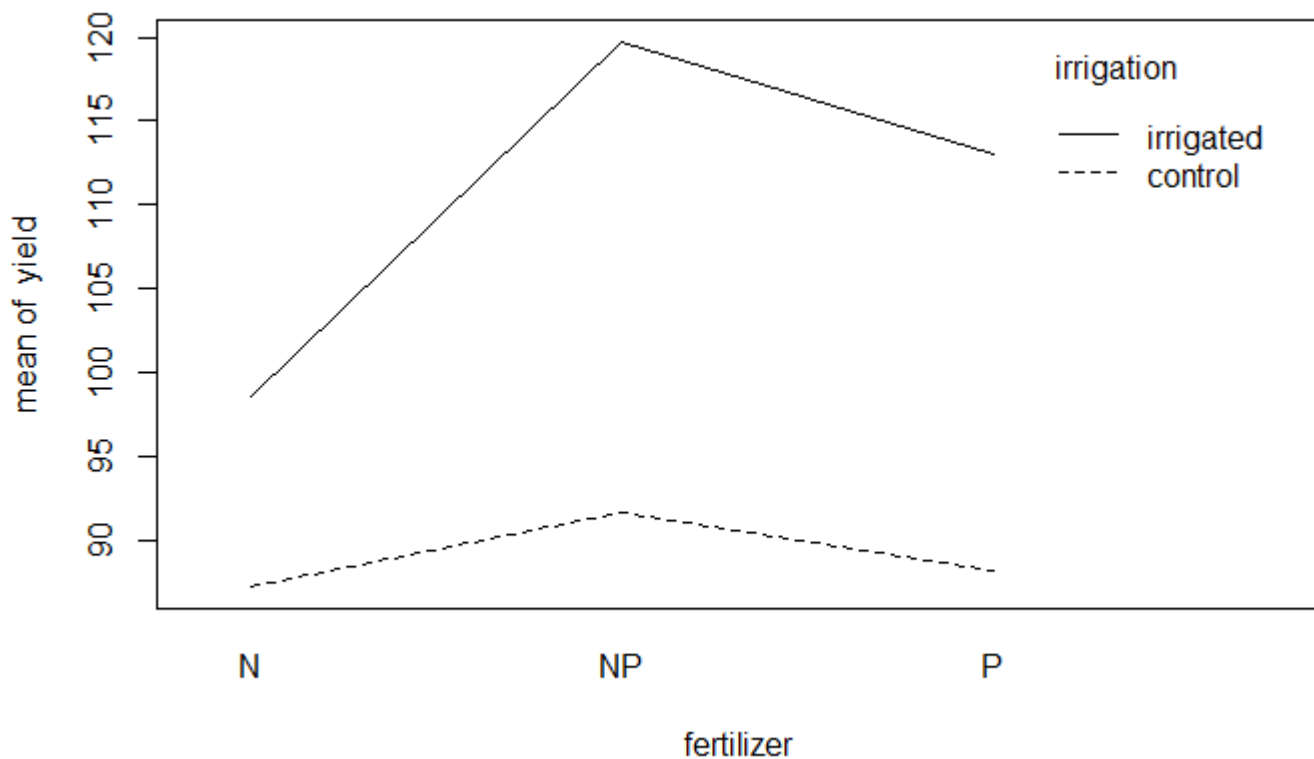
[Hide](#)

```
yields <- read.table("splityield.txt",header=T)
attach(yields)
names(yields)
```

```
[1] "yield"      "block"      "irrigation" "density"    "fertilizer"
```

[Hide](#)

```
interaction.plot(fertilizer,irrigation,yield)
```

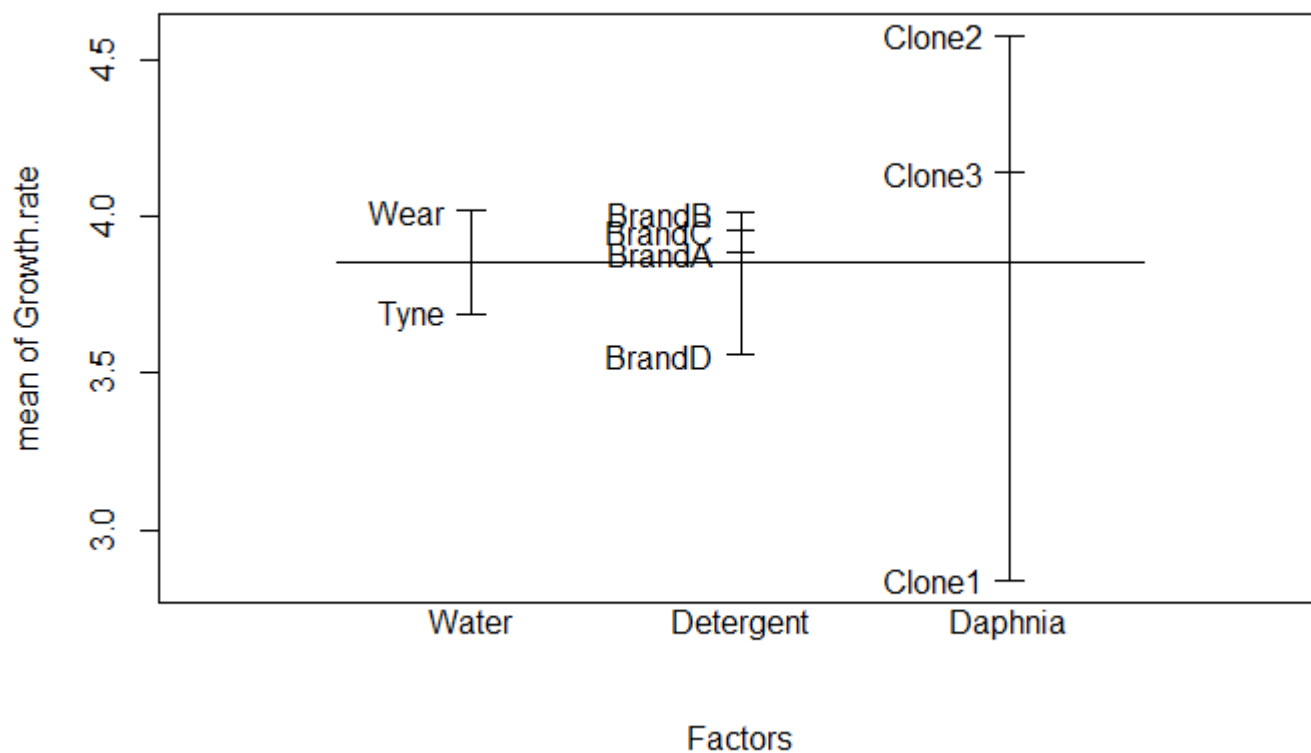
[Hide](#)

NA
NA

Section 5.9.1

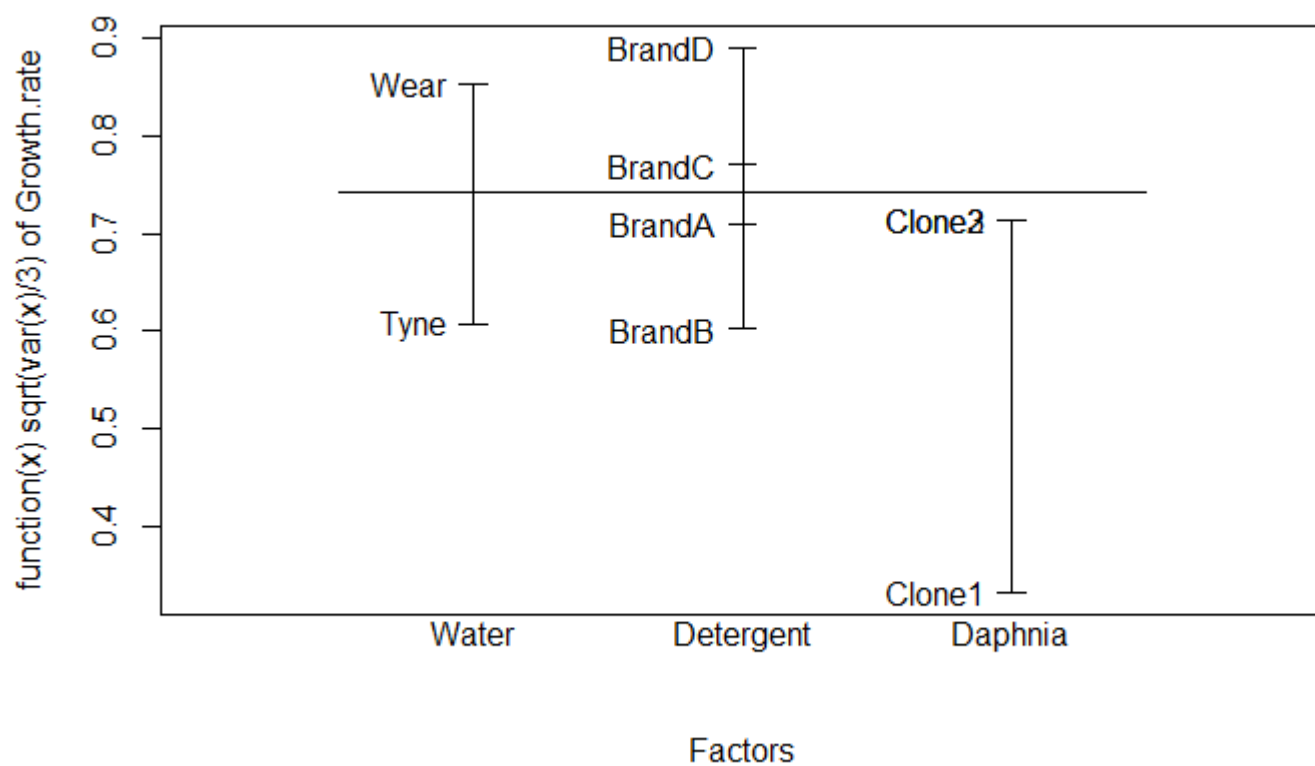
Hide

```
plot.design(Growth.rate~Water*Detergent*Daphnia)
```



Hide

```
plot.design(Growth.rate~Water*Detergent*Daphnia,
  fun=function(x) sqrt(var(x)/3) )
```



Section 5.9.2

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

[Hide](#)

```
bubble.plot <- function(xv,yv,rv,bs=0.1){  
  r <- rv/max(rv)  
  yscale <- max(yv)-min(yv)  
  xscale <- max(xv)-min(xv)  
  plot(xv,yv,type="n", xlab=deparse(substitute(xv)),  
       ylab=deparse(substitute(yv)))  
  for (i in 1:length(xv)) bubble(xv[i],yv[i],r[i],bs,xscale,yscale) }  
bubble <- function (x,y,r,bubble.size,xscale,yscale) {  
  theta <- seq(0,2*pi,pi/200)  
  yv <- r*sin(theta)*bubble.size*yscale  
  xv <- r*cos(theta)* bubble.size*xscale  
  lines(x+xv,y+yv) }  
  
ddd <- read.table("pgr.txt",header=T)  
attach(ddd)
```

The following objects are masked from data (pos = 23):

FR, hay, pH

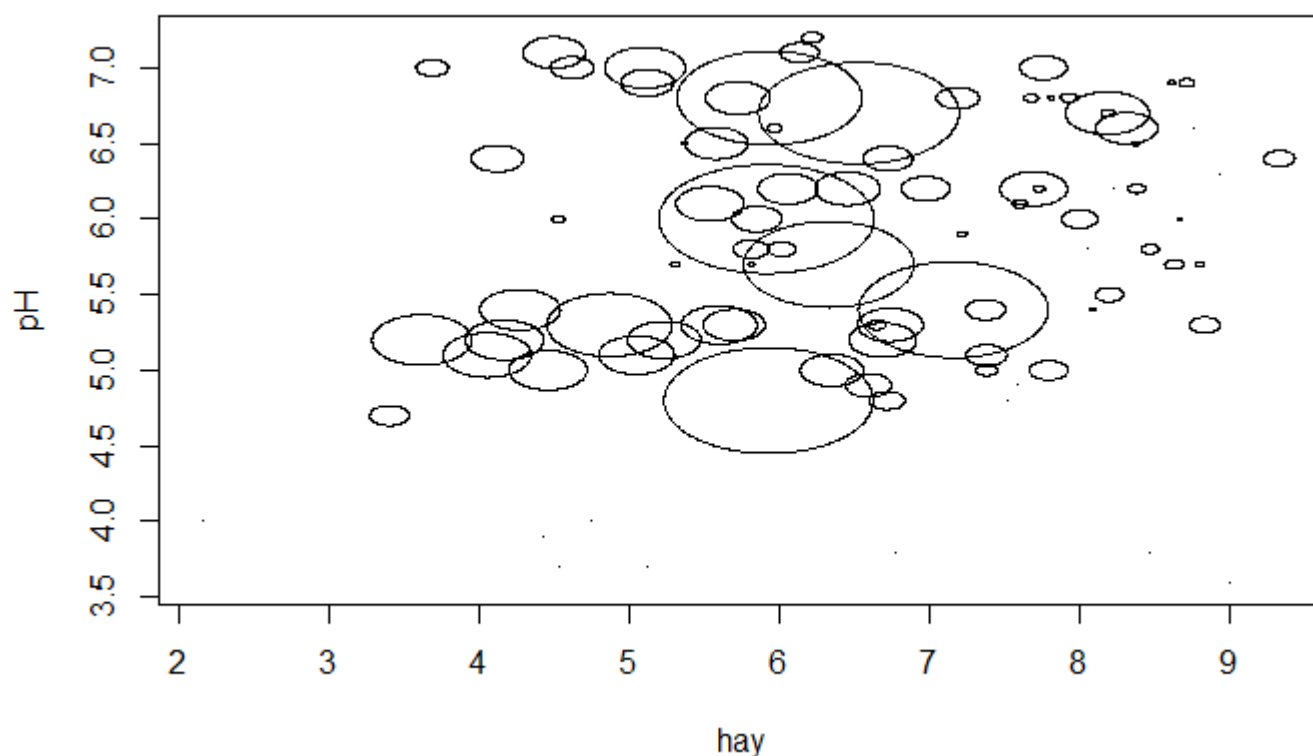
[Hide](#)

```
names(ddd)
```

```
[1] "FR"  "hay" "pH"
```

[Hide](#)

```
bubble.plot(hay,pH,FR)
```



Section 5.9.3

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

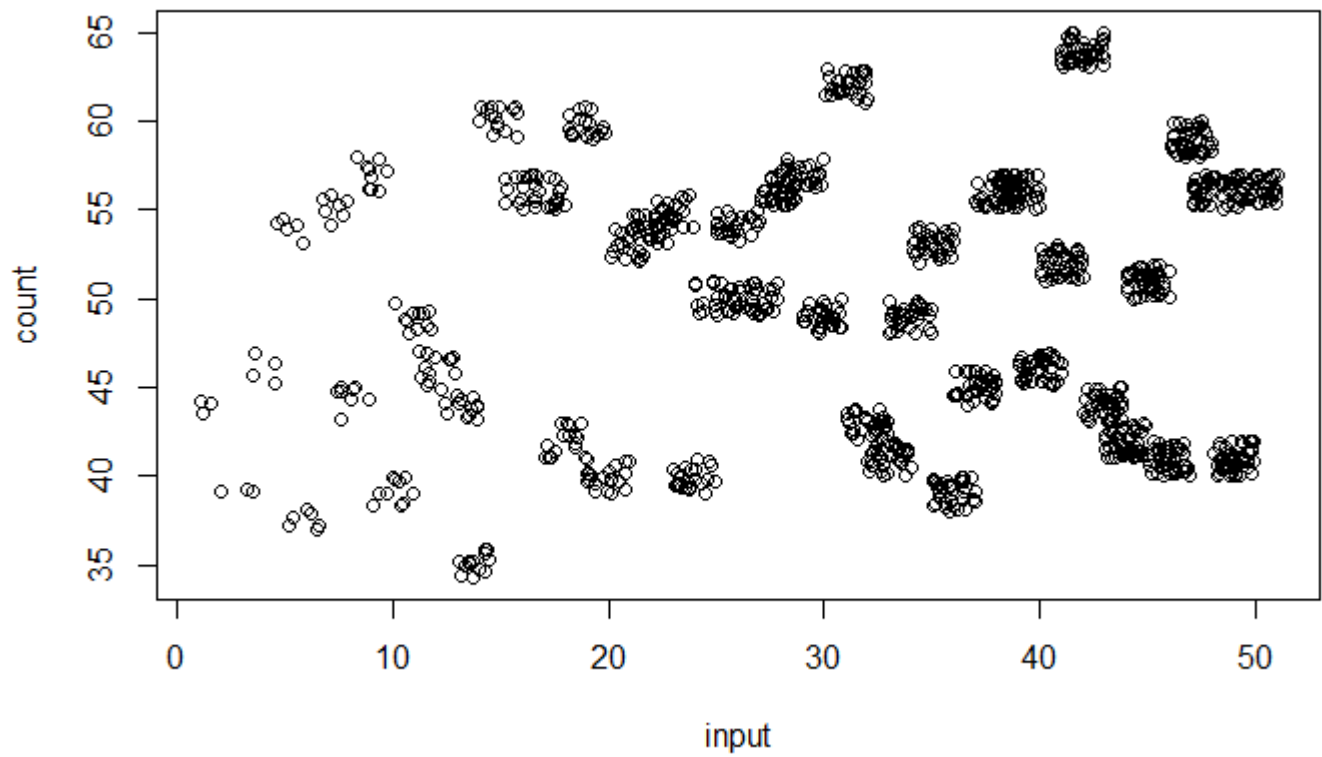
[Hide](#)

```
numbers <- read.table("longdata.txt",header=T)
attach(numbers)
names(numbers)
```

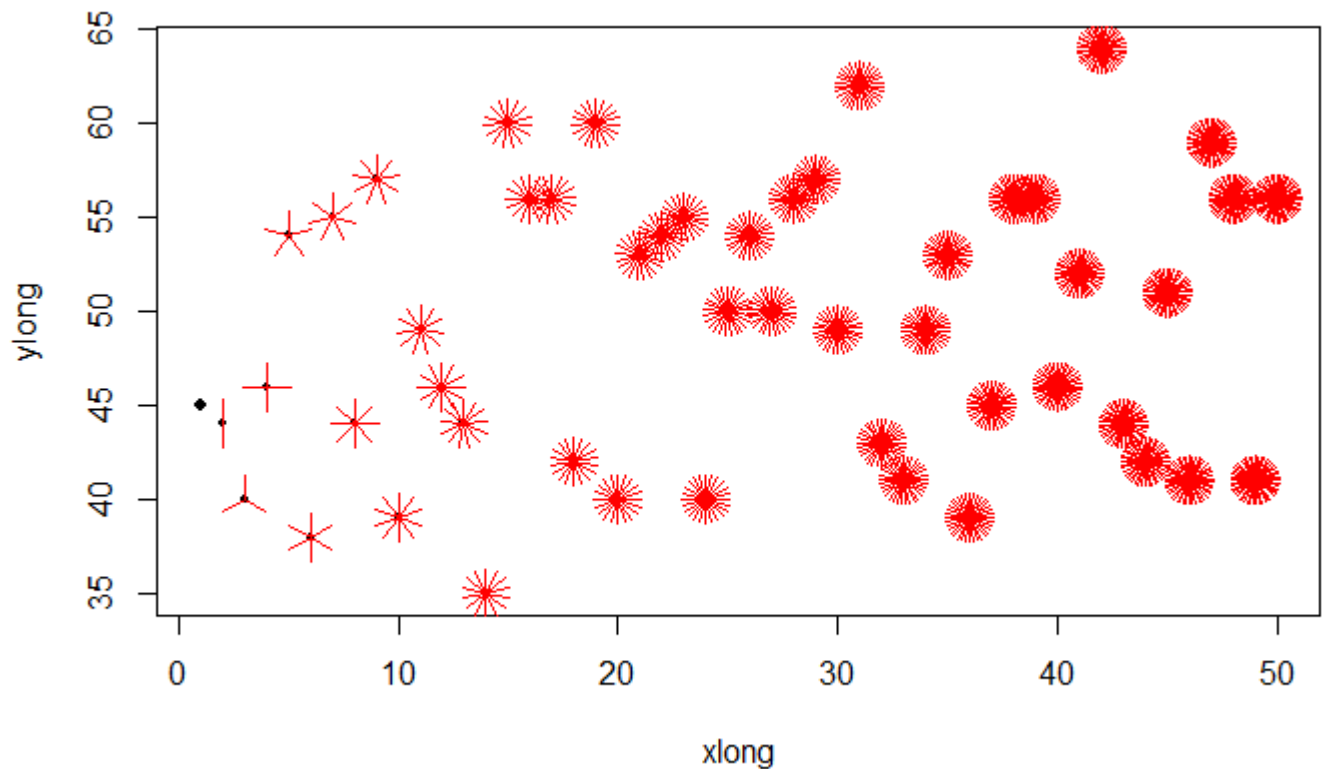
```
[1] "xlong" "ylong"
```

[Hide](#)

```
plot(jitter(xlong,amount=1),jitter(ylong,amount=1),xlab="input",ylab="count")
```

[Hide](#)

```
sunflowerplot(xlong,ylong)
```



Section 5.10

[Hide](#)

```
setwd("C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook")
```

The working directory was changed to C:/Users/Nathan/Desktop/Important Docs/school/stats db/therbook inside a notebook chunk. The working directory will be reset when the chunk is finished running. Use the knitr root.dir option in the setup chunk to change the working directory for notebook chunks.

[Hide](#)

```
data <- read.table("pollute.txt",header=T)
attach(data)
```

The following objects are masked from data (pos = 19):

Industry, Pollution, Population, Rain, Temp, Wet.days, Wind

The following objects are masked from data (pos = 20):

Industry, Pollution, Population, Rain, Temp, Wet.days, Wind

[Hide](#)

```
pdf("pollution.pdf",width=7,height=4)
par(mfrow=c(1,2))
plot(Population,Pollution)
plot(Temp,Pollution)
```

[Hide](#)

```
dev.off()
```

```
null device
      1
```

[Hide](#)

```
postscript("pollution.ps",width=7,height=4)
par(mfrow=c(1,2))
plot(Population,Pollution)
```

[Hide](#)

```
plot(Temp,Pollution)
dev.off()
```

null device
1